108.0001



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:

Jeffry L. Eakin

Serial No.:

09/619,411

Filed:

July 19, 2000

For:

METHODS AND APPARATUS FOR PROCESSING AND DISTRIBUTING

INFORMATION RELATING TO COSTS AND SALES OF PRODUCTS

Group:

2753

Examiner:

Not Assigned Yet.

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D.C. 20231, on the date set forth below:

Signed: All Last Mark

Name: Tlynthia Jordan

Date: October 4, 2000

Chapel Hill, North Carolina October 4, 2000

Assistant Commissioner of Patents and Trademarks Washington, DC 20231

RESPONSE TO NOTICE TO FILE MISSING PARTS OF NONPROVISIONAL APPLICATION

Sir:

Enclosed is a copy of the Notice to File Missing Parts of Nonprovisional Application and Declaration and Power of Attorney for the above identified case.

Also enclosed is our check in the amount of \$130 to cover the fee.

ر نړو

Respectfully submitted,

Peter H. Priest

Reg. No. 30,210 Law Offices of Peter H. Priest 529 Dogwood Drive Chapel Hill, NC 27516 (919) 942-1434





United States Patent and Trademark Office

COMMISSIONER FOR PATENTS UNITED STATES PATENT AND TRADEMARK OFFICE WASHINGTON, D.C. 2023I

www.uspto.gov

APPLICATION NUMBER

FILING/RECEIPT DATE

FIRST NAMED APPLICANT

ATTORNEY DOCKET NUMBER

09/619,411

07/19/2000

Jeffrey Lynn Eakin

108.0001

Peter H Priest Law Offices of Peter H Priest 529 Dogwood Drive Chapel Hill, NC 27516



FORMALITIES LETTER

OC000000005394773

Date Mailed: 09/13/2000

NOTICE TO FILE MISSING PARTS OF NONPROVISIONAL APPLICATION

FILED UNDER 37 CFR 1.53(b)

Filing Date Granted

An application number and filing date have been accorded to this application. The item(s) indicated below, however, are missing. Applicant is given TWO MONTHS from the date of this Notice within which to file all required items and pay any fees required below to avoid abandonment. Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a).

- The oath or declaration is missing.
 A properly signed oath or declaration in compliance with 37 CFR 1.63, identifying the application by the above Application Number and Filing Date, is required.
- To avoid abandonment, a late filing fee or oath or declaration surcharge as set forth in 37 CFR 1.16(e) of \$130 for a non-small entity, must be submitted with the missing items identified in this letter.
- The balance due by applicant is \$ 130.

copy of this notice MUST be returned with the reply.

Customer Service Center

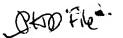
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE

16/11/2000 UABRHAH1 00000006 09619411

01 FC:105

130.00 OP





United States Patent and Trademark Office

COMMISSIONER FOR PATENTS United States Patent and Trademark Office WASHINGTON, D.C. 20231

IND CLAIMS APPLICATION NUMBER GRP ART UNIT FIL FEE REC'D ATTY.DOCKET.NO **DRAWINGS** TOT CLAIMS FILING DATE 2761 708 108,0001 25 21 07/19/2000 09/619.411

Peter H Priest Law Offices of Peter H Priest 529 Dogwood Drive Chapel Hill, NC 27516



FILING RECEIPT



Date Mailed: 09/13/2000

Receipt is acknowledged of this nonprovisional Patent Application. It will be considered in its order and you will be notified as to the results of the examination. Be sure to provide the U.S. APPLICATION NUMBER, FILING DATE, NAME OF APPLICANT, and TITLE OF INVENTION when inquiring about this application. Fees transmitted by check or draft are subject to collection. Please verify the accuracy of the data presented on this receipt. If an error is noted on this Filing Receipt, please write to the Office of Initial Patent Examination's Customer Service Center. Please provide a copy of this Filing Receipt with the changes noted thereon. If you received a "Notice to File Missing Parts" for this application, please submit any corrections to this Filing Receipt with your reply to the Notice. When the PTO processes the reply to the Notice, the PTO will generate another Filing Receipt incorporating the requested corrections (if appropriate). Corec X

Applicant(s)

Jeffrey Lynn Eakin, Residence Not Provided; Christopher Huyette Howe, Residence Not Provided; Joseph Eric Lipovich, Residence Not Provided; Mark Wesley, Residence Not Provided; Michael James Platt, Residence Not Provided;

mac KENZIE

Continuing Data as Claimed by Applicant

Angua april 1944

Foreign Applications

If Required, Foreign Filing License Granted 09/12/2000

Title

Methods and apparatus for processing and distributing information relating to cost and sales of products COSTS

Preliminary Class

705

108.0001



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Declaration and Power of Attorney

As the below named inventors, we hereby declare that:

Our residence, post office address and citizenship are as stated below next to our names.

We believe we are the original, first and joint inventors of the subject matter which is claimed and for which a patent is sought on the invention entitled METHODS AND APPARATUS FOR PROCESSING AND DISTRIBUTING INFORMATION RELATING TO COSTS AND SALES OF PRODUCTS, the specification of which was filed on July 19, 2000 as U.S. Serial No. 09/619,411.

We hereby state that we have reviewed and understand the contents of the above identified specification, including the claims, as amended by an amendment, if any, specifically referred to in this oath or declaration.

We acknowledge the duty to disclose all information known to us which is material to patentability as defined in Title 37, Code of Federal Regulations, 1.56.

We hereby claim foreign priority benefits under Title 35, United States Code, 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

None

We hereby claim the benefit under Title 35, United States Code, 119(e) of any United States provisional application(s) listed below:

None

We hereby claim the benefit under Title 35, United States Code, 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, 112, we acknowledge the duty to disclose all information known to us to be material to patentability as defined in Title 37, Code of Federal Regulations, 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

None.

We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any

patent issued thereon.

We hereby appoint the following attorney with full power of substitution and revocation, to prosecute said application, to make alterations and amendments therein, to receive the patent, and to transact all business in the Patent and Trademark Office connected therewith:

Peter H. Priest

(Reg. No. 30,210)

Please address all correspondence to Peter H. Priest, Law Offices of Peter H. Priest, 529 Dogwood Drive, Chapel Hill, North Carolina 27516. Telephone calls should be made to Peter H. Priest by dialing Area Code 919-942-1434.

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Citizenship:

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huitoph-Hyette-Hose Date:

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Inventor's signature

_

g fur hour Date: 9/25/00

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Lun	name	O1 70	μ	ши	HIVOH	w.

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Inventor's signature

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Citizenship:

US

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FILE REFERENCE: 108627.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1090-03-24
PRIOR PILING DATE: 1990-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR TILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-09
PRIOR TILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR TILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 137060, Application US/10027632 Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
-10-027-632-137060
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Pred. No. 1.6e-33;
1; Mismatches 42; Indels 11;
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Maximum Match 100%
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1: 9b
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Gapop 10.0 , Gapext 1.0
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11829.554 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AQ527649 RPCI-11-3
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CR773823 DXFZ24591
BM667682 UI-E-DXO-
AIT73373 CO13a11.X
AQ314507 RPCII-11-2
BM95430 UI-H-DFO-
AQ415039 RPCI-11-2
BM993430 UI-H-DFO-
AQ415039 RPCII-10
BU626395 UI-H-DFO-
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CR607576 full-H-DFO-
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805 TCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAACGTTGTCTCTACT 864	308 GGCTGGGTATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGTGGA 249	745 GGCTGGGCGCATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGGCCGAAGGCAGGTGGA 804	Query Match 19.2%; Score 199.2; DB 5; Length 658; Best Local Similarity 82.0%; Pred. No. 4e-22; Matches 246; Conservative 0; Mismatches 43; Indels 11; Gaps 1;	/mol_type="mRNA" /db_xref="tsxon:4530" /clone="y722903p3" /clone_lib="Oryza sativa library (Han B)" ORIGIN	source 1658 /organism="Oryza sativa"	FEATURES Location/Qualifiers	Clone requests: bhan@ncgr.ac.cn This is rice cdna est clone Wob cite. http://www.ncgr.ac.cn	bhan@ncgr.ac.cn	Chinese Academy of Sciences	COMMENT Confact: Han Bin		Weng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T.,	Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.	REFERENCE I (Dases I to 658) Alffredes Han B. Feng O. Hijang Y.C. Ying K. I.i.Y. Gjan J.P. Zhu J.J.	Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	OKGANISM OTyza sativa		S EST.		y722g03p3, mRNA sequence.	DEFINITION BX928516 Oryza sativa library (Han B) Oryza sativa cDNA clone	TAGE TO AND THE TAGE TO THE TA	RESULT 1

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12743 row: h column: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1024)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT_6641246 NIH_MGC_68 Homo sapiens cDNA clone 5', mENA sequence.
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                                       TTTTCGTTTTGAGATGAAGATACTTAGTTTTAGTCCAGGGGCTGGGCGCGATAGCTGATG 765
                                                                           CAGGTAAGATAGGCTTTCTCTCTCTCCCTATACCAAGTAATTTATACCTACACAGATTGGGC
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                                                                                                                                                                                                                                                                                                                    /tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo c
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
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/db_xref="taxon:9606"
/clone="IMAGE:5735872"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-Merck EST Project
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Other ESTs: zo19c03.x5
Other ESTs: zo19c03.x5
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                                                                                                                                                                                                                                                                                                                                                                                          correct orientation)
Insert Length: 1908 Std Error: 0.00
Seq primer: -40RP from Gibco
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                                           /db_xref="taxon:9606"
/clone="IMAGE:587332"
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|db_xref="GDB:4619634"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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76.9%;
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Pred.
196.4; DB 1;
No. 1.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
fisue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 12-301, >ALU (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ004374 621 bp mRNA JUI-H-EIO-ayn-j-13-0-UI.81 NCI_CGAP_EIO Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BQ004374.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAACATGGTGAAACGTTGTCTCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTCCATCTCAAAAAAAAAAAAAAAAAAACTCGA 13
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/clone="MAGE::841132"
/clone="TMAGE::841132"
/tlssue_type="Chondrosarcoma"
/dev stage="Adult"
/dev stage="Adult"
/lab host="BH108 (Life Technologies)"
/clone_lib="NCI_CGAP_EIO"
/clone_11b="NCI_CGAP_EIO"
/note="Organ: Left Pelvis Vector: pT7T3-Pac (Pharmacia)
/note="Organ: Left Pelvis Vector: pT7T3-Pac (Pharma
                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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primer: M13 FORWARD

ocation/Qualifiers

/db_xref="taxon:9606" /clone="IMAGE:5874920" /tissue_type="Lung Focal Fibrosis"

/organism="Homo sapiens" /mol_type="mRNA"

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   745 GGCTGGGCGCGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGCCGAGGCAGGTGGA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244;
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-27, >AT_rich#Low_complexity 133-417, >ALU (matched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ017611
BQ017611.1 GI:19752888
                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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UI-H-DIO-auv-j-09-0-UI.61 NCI_CGAP_DIO I
IMAGE:5874920 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATCTGAGGTCAGGAGTTCGAGACCAGCCTGGACAACATGGTGAAACCCTGTCTCTGCT
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Pred. No. 1.3e-21;
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TITLE
JOURNAL
COMMENT
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ORGANISM
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                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleon Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 559)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and T., Tan, F., Waterston, R., Williamson, A., Wohldmann, P. and T., Tan, F., Tan, F., Tan, F., Tan, F., Tan, F., Waterston, R., Williamson, A., Wohldmann, P. and T., Tan, F., Tan, F., Tan, F., Tan, F., Tan, F., Waterston, R., Williamson, A., Wohldmann, P. and T., Tan, F., Tan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
T78471
             Unpublished (1995)
Other_ESTs: yd68f03.r1
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 bp mR
Vd68f03.sl Soares fetal liver spleen
IMAGE:113405 3' similar to accompany
                                                                            The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T78471.1 GI:696980
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_DI0"
/clone_lib="NCI_CGAP_DI0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_DI0 is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_SEQ=ATACGCGGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3' similar to contains Alu repetitive element, marris
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_LIB=UI-H-DIO
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Pred. No. 1.5
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1.5e-21;
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ORIGIN

REFERENCE AUTHORS

ACCESSION VERSION

KEYWORDS

RESULT 6 T78471/c

S 멍 Ś 밁 5 В 8 밁 Ś 밁 Ś

FOCUS

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RESULT 7
AQ527649
LOCUS
                       DEFINITION
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                                                                                                                         11
                                                                                                                                                                                           71
AQ527649 456 bp DNA RPCI-11-348021.TV RPCI-11 Homo sapiens (RPCI-11-348021, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
Insert Size: 632
Insert Size: 632
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 632
Std Error: 0.00
Seg primer: -21m13
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                                                                                                                       CAAAACAAA 3
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                                                                                                                                                                                                                                                                                                                        AGTTAAGCCCCCATCTCTACTAAAAATACAAAAATTGGCCAGGCATGGTGGCGGGCACCTG
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                                                                                                                                                                                                                                                                                                                                                                                           GTGAGGCCGACGCAGGTGGATCACTTGAGGTCA-GAATTTGAGACCAGCCTGGCCAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:469022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:113405"
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Pred. No. 1.6e-21;
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                linear
genomic clone
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                                   GSS 18-MAY-1999
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Best Local Similarity
Matches 252; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Other GSSs: RPCI-11-348021.TJ
Other GSSs: RPCI-11-348021.TJ
Contact: Shaying Zhao, William Nierman, Ma
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 208
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                 961
                                                                                                                                                           239
                                                                                                                                                                                              901
                                                                                                                                                                                                                                       179
                                                                                                                                                                                                                                                              841 ACATGGTGAAACGTTGTCTCTACTAAAAATACAAAAATTAGACAGGGGTGGTGGCACACA
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359
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                                                                                                                                                                                                                                                                                                                                                                                                                                        721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 456)

Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ527649
AQ527649.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATACTTAGTTTTAGTCCAGGGGCTGGGCGCGATAGCTGATGCCTGTGGTCCCAGTG
                            TTGTCTCAAAAAAAAAAAAAAA 1032
                                                                                                                 AGGTTGCAGTGAG------CCATTGCACTCCAGCCTGGGCAACACAGTGAGACTC
                                                                                                                                                                                                TCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAG
                                                                                                                                                                                                                                       ACATGGCGAAACCCCGTCTCCACTAAAAATACAAAAATTAGTCAGGCGTGGTGGCATGTG
                                                                                                                                                                                                                                                                                                                  CTTTGGGAGGCCGAGGCGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGCCA
  CTGTCTCAAAAAAATCTAAAAA 381
                                                                              AAGTTGCAGTGAGCCGAGATCGCACCACTGCAGTCCAGCCTGGGTAACAAAGCGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="GDB:7633604"
/db_xref="taxon:9606"
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Pred. No. 2.1e-21;
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Unpublished (1997)
Other GSSs: RPCI-11-235F3.TJ
Contact: Shaying Zhao, William Nierman, Ma
Department of Eukaryotic Genomics
The Institute for Genomic Research
o712 Medical Center Dr., Rockville, MD 20
                                                                                                                                                                                                                                               805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hbe@tigr.org
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or {
Research Genet cs (info@resgen.com). BAC end search page:

Research Genet cs (info@resgen.com) BAC end search/bac_end_search.)
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 838 0200 Fax: 301 838 0208
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RPCI-11-235F3.TV RPCI-11
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Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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GSS.
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                          AAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCTACTCAGGAG
GCTGAGAGAGAGAATTGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCACTGCACTC
                                                                                                    GCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCATTGCACTC
                                                                                                                                         AAAAATACAAAAATTAGCTGGGCGTGGTGGCAGGCTCTTGTAGTCCCAGCTACTCGGGGG
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA
/db_xref="GDB:7589978"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RPCI-11-235F3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rl sequence also available.
This clone (DKFZp686D0380) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 3' sequence of the clone insert Clone from S. Wiemann, Molecular Genme Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@Akfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, theidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX490431 681 bp mRNA DKFZp686D0380 s1 686 (synonym: hlcc3) HcDKFZp686D0380 3', mRNA sequence. BX490431 GI:3199889
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Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                        GAGCCAAGGTCGCGCCATTGCACTCCAGCCTGGGCGACAGAGTGACACTTCTCAAAAAAAC
                                                                                                                                                      GA------GCCATTGCACTCCAGCCTGGGCAACACAGTGAGACTCTTGTCTCAAA 1019
                                                                                                                                                                                                                     CAGCTACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGT
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                                                                                                                                                                                          CCAAGGCAGGTGGATNACCTGAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA
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/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686D0380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dev_stage="adult"
lab_host="DH10B"
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RESULT 11 BM667682/c

DEFINITION

BM667682 504 bp mRNA lines UI-E-DX0-ags-f-14-0-UI.81 UI-E-DX0 Homo sapiens UI-E-DX0-ags-f-14-0-UI 3', mRNA sequence.

CDNA

EST 27-FEB-2002

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 74
                                                                                                                                                                                                                                                                                                                                                                                                                        250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID-DKFZp459I2062 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 452)
KOehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Os. Fobo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Koehrer, K., Beyer, A., Mewes, H.W., Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MIPS
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CR773823.1 GI:52617096
EST.
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DKFZp459I2062_rl 459 (synonym: p

DKFZp459I2062_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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                     TCTTGTCTCAAAAAAAAA 1026
                                                                                                                                     TGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCACTTGAACCCCGGGAGGC
                                                                                                                                                               CATCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAAATTCCTTGAACCTGGGAGGC
                                                                                                                                                                                                                                            CAACATGGTGAAACGTTGTCTCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACA 898
                                                                                                                                                                                                                                                                             CATTTTGGGAGGCCAAGGCAGGTGGATCAACTGAGGTCAGGAGTTTGAGACCAGCCTGAC
                                                                                                                                                                                                                                                                                                   TGCTTTGCGGGGCCGAGGCAGGCAGGAGTCACTTAAGGTCAGGAGTTTTGAGACCAGCCTGCC 838
                                                                                                                                                                                                                                                                                                                                                                               ATGAAGATACTTAGTTTTAGTCCAGGGGGTGGGCGCGATAGCTGATGCCTGTGGTCCCAG
                                                                   AGAGGTTGCAGTGAGCCAAGATCACGCCATTGCACTCCAGCGTGGGCAACAGAGTGAGCC
                                                                                                      AGAGGTTGCAGTGA-----
                                                                                                                                                                                                                                                                                                                                                ATGAGTATTAATTAAGAGAGGGCAGGCTGGGCACGTTAGTTCACGCCTGTAATCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="DKFZp45912062"
/clssus_type="cortex"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
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56
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 194.2; DB 7
Pred. No. 2.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                         -GCCATTGCACTCCAGCCTGGGCAACACAGTGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                      58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SfilA; Site_2:
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ORGANISM
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                  731 AGTTTTAGTCCAGGGGCTGGGCGCGATAGCTGATGCCTGTGGTCCCAGTGCTTTTGCGGGG 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-27, >AT_rich#Low_complexity 132-416, >ALU (matched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discovery
Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8889548
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1 (bases 1 to 504)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYA-Yes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                 Similarity
                                             CCGAGGCAGGTGGATCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAA 850
                                                                                                                                                    AATATGTGTGTATAGGCTGGGTGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGG 371
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer: M13 Forward
                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone lib="UI-B-DXO"

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/tissue_type="fetal eyes"
/dev_stage="fetal eyes"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type= "max.../db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ=AGAATCAAGA"
                                                                                                                                                                                                                                                                                                Score 194.2; DB 4;
Pred. No. 2.7e-21;
"" matches 58;
                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 504;
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311
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731 AGTTTTAGTCCAGGGGCTGGGCGCGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGG 790

Query Match Best Local Similarity Matches 250;

18.7%;

DB 1;

Conservative

0; Mismatches Score 194.2; DB 1 Pred. No. 2.7e-21;

Indels Length 515;

11;

Gaps

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JOURNAL COMMENT
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AUTHORS
TITLE
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AI073373/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI073373 515 bp mRNA linear ool3all.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens IMAGE:1566044 3' similar to contains Alu repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 515)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                     /clone_libe_Soares_NSF_F8_9W_OT_PA_P_S1"
/clone_libe_Soares_NSF_F8_9W_OT_PA_P_S1"
/clone_libe_Soares_NSF_F8_9W_OT_PA_P_S1"
/clone_libe_Soares_NSF_F8_9W_OT_PA_P_S1"
/clone_libe_Soares_NSF_F8_9W_OT_PA_P_S1"
/clone_libe_Soares_NSF_F8_9W_OT_PA_P_S1"
a modified_polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified_cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NHSF pool 1:
130384-310919, 323208-325895 Soares NHSF pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NbHF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1566044"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: RPCI11-103B6.TJ
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
 Similarity
                                                                                                                                                                                                                                                                                          Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ĀQ314507.1 GI:4045970
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301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                        hbe@tigr.org
                                                                                                                                                            /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="GDB:7539197"
/db xref="taxon:9606"
/clone="RPCI-11-103B6"
                                                                    /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male_BAC_Library"
                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                 sex="Male"
18.7%;
79.8%;
Score 194.2; DB 8; Pred. No. 2.7e-21;
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                                                                                       EcoRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soaresgations, edu The following repetitive elements were found in this cDNA sequence: 1-27, ATTich#Low complexity (matched compliment) 133-417, PAU (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 724)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 bp mRNA
UI-H-DF0-beu-o-10-0-UI.s1 NCI CGAP DF0 H
UI-H-DF0-beu-o-10-0-UI 3', mRNA sequence
BU626395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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/clone_lib="NCI_CGAP_DF0"
//clone_lib="NCI_CGAP_DF0"
//clone="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of
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/db xref="taxon:9606"
/clone="UI-H-DF0-beu-o-10-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="PHH10B (Life_Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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Best Local Similarity
Bource
                                                                                                                                                                                                               Unpublished (1997)

Other GSSe: RPCI-11-203E9.TV

Other GSSe: RPCI-11-203E9.TV

Contact: Shaying Zhao, William Nierman, Ma

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 208

Tel: 301 838 0208

Fax: 301 838 0208
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                               Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
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1 (bases 1 to 540)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
Venter,J.C.
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Use of BAC End Sequences from
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TAG_TISSUE-subchondral bone
TAG_LIB-UI-H-DF0
TAG_SEQ-GTTAAGCGTC"
                  Location/Qualifiers
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/mol type="genomic DNA"
/db xref="taxon:9606"
/clone="RPCI-11-203E9"
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/clone lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1:
RPCII1 Human Male BAC Library"
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1: /cgn2_6/ptodatta/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatta/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatta/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodatta/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                              US-09-482-273-180
US-09-318-930-313
US-09-312-283C-313
US-09-312-283C-313
US-09-247-155-90
US-09-247-155-90
US-09-270-767-48558
US-09-270-767-4854
US-09-270-767-4854
US-09-264-227A-3
US-09-264-227A-3
US-09-264-227A-3
US-09-264-901-16
US-09-264-901-12
US-09-265-901-14
US-09-265-901-14
US-09-265-901-17
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           180, App
313, App
3116, App
90, App
1116, App
9115, App
33341, A
48584, A
54854, A
558854, A
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US-09-482-273-180
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49 18.8 118 4 US-09-270-767-6231 49 18.8 154 4 US-09-248-796A-20059 49 18.8 223 4 US-09-265-901-36 49 18.8 348 4 US-09-270-767-46628 49 18.8 373 4 US-09-248-796A-17973 49 18.8 373 4 US-09-248-796A-17973 49 18.8 462 3 US-09-621-976-5389 48 18.5 125 4 US-08-469-260A-412 48 18.5 125 4 US-08-469-260A-412 48 18.5 125 4 US-08-467-344A-412 48 18.5 125 4 US-08-467-344A-412 48 18.5 125 4 US-08-486-452 48 18.5 125 4 US-08-808-550-35 48 18.5 213 2 US-08-808-550-35 48 18.5 213 4 US-09-925-901-42 48 18.5 307 4 US-09-925-901-42 48 18.5 307 4 US-09-925-940-113 48 18.5 315 4 US-09-925-940-113 48 18.5 316 4 US-09-252-991A-29961	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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	29961, A	113, App	3, Appli	7121, Ap	15716, A		⊳	412, App	•	412, App	412, App	5389, Ap	1, Appli	17973, A	46628, A	36, Appl	20059, A	62231, A

ALIGNMENTS

; LENGTH: 49 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-482-273-180 CURRENT APPLICATION NUMBER: US/09/482,273 CURRENT FILING DATE: 2000-01-13 EARLIER APPLICATION NUMBER: PCT/US99/15849 EARLIER FILING DATE: 1999-07-14 EARLIER APPLICATION NUMBER: 60/92,921 EARLIER FILING DATE: 1998-07-15 EARLIER APPLICATION NUMBER: 60/092,922 EARLIER APPLICATION NUMBER: 60/092,922 EARLIER FILING DATE: 1998-07-15 EARLIER APPLICATION NUMBER: 60/092,956 EARLIER FILING DATE: 1998-07-15 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 180 LENGTH: 49 Sequence 180, Applic Patent No. 6534631 GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: 71 Human Secreted Proteins FILE REFERENCE: PZ030P1 Application US/09482273

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Sequence 313, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Onrust, Rene

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09
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US-09-188-930-313
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Length 49; Indels

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CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
FEARLIER APPLICATION NUMBER: PCT/US99/15849
FEARLIER FILING DATE: 1999-07-14
FEARLIER FILING DATE: 1998-07-15
FEARLIER APPLICATION NUMBER: 60/092,921
FEARLIER APPLICATION NUMBER: 60/092,922
FEARLIER FILING DATE: 1998-07-15
FEARLIER FILING DATE: 1998-07-15
FEARLIER APPLICATION NUMBER: 60/092,956
FEARLIER APPLICATION NUMBER: 60/092,956
FEARLIER APPLICATION NUMBER: 60/092,956
FEARLIER FILING DATE: 1998-07-15
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; ORGANISM: Human
US-09-188-930-313
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LENGTH: 70
TYPE: PRT
ORGANISM: Mouse
               NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 116
LENGTH: 71
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TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
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APPLICANT:
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Best Local S
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SOFTWARE: FastSEQ for
SEQ ID NO 313
LENGTH: 70
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CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
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TYPE: PRT
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Sleeman, Matthew
Onrust, Rene
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for Windows Version
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Pred. No. 1e-28;
Mismatches
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Pred. No. 1e-28;
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; NAME/KEY: SIGNAL
; LOCATION: -71..-1
US-09-247-155-90
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                                                               APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
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                                                                                                                                                                                                                  Sequence 8115, Application US/09513999C Patent No. 6783961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local (
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               PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
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 SOFTWARE:
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CURRENT FILING DATE: 1999-02-09
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 1.6e-28;
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Pred. No. 1e-28;
                                                                                                                                             and
                                                                                                                                             Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 106;
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RESULT 9

US-09-200-767-39637

; Sequence 39637, Application US/09270767

; Patent No. 6703491
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TITLE OF INVENTION: Nucleic acids and proteins of
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 48558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 33341
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48558, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION:
                                                                                                                                                                   Matches
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Best Local Similarity
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Best Local :
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LENGTH: 106
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                                                                                                                                                                                                                                                                                 LENGTH: 114
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                                                                                                   43
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                                                                                                 MNILGMIFSMCGLMMKLKWCAWFALYCSCISFASSRASDDAKQVLSSFM 91
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77.6%;
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Pred. No. 1.6e-22;
8; Mismatches 3
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Pred. No. 1.6e-22;
8; Mismatches 3
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Pred. No. 1.6e-28;
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CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 199-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 322
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                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09254227A Patent No. 6696257 GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54884
LENGTH: 240
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER: OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39637
LENGTH: 240
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APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Prottein-Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1898
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ORGANISM: Drosophila melanogaster
FEATURE:
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13; Conserv
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; SOFTWARE: PatentIn veri
; SEQ ID NO 3
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-3
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APPLICANT: Yau, King-Wai
APPLICANT: Yau, King-Wai
APPLICANT: Krautwurst, Dietmar
TITLE OF INVENTION: Olfactory Receptor Expession Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-254-227A-3
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                                                                             ; OTHER INFORMATION: PCR US-09-465-901-16
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US-09-465-901-16
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Best Local Similarity 23.2
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Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                        SEQ ID NO 16
LENGTH: 223
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Best Local Similarity
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APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
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ORGANISM: Homo sapiens
                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 LVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSF 278
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  20.4%; ilarity 31.8%; Conservative 1
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23.2%; Pred. No. 15;
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  Score 53; DB 4;
Pred. No. 16;
l2; Mismatches 1
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    16;
                                    Length 223;
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US-09-248-796A-25087
US-09-248-796A-25087, Application US/09248796A

Sequence 25087, Application US/09248796A

; Patent No. 6747137
; GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANTION: FOR DIAGNOSTICS AND THERAPEUTICS

FITTLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 25087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25087
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Search completed: March Job time: 60 secs
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APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 15809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15809, Ap
Patent No. 6747137
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                  ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                       TYPE: PRT
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les 12; Conserv
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Pred. No. 5.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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260
1 MNLLGMIFSMCGLMLKLKWC.....ISFANSRSSEDTKQMMSSFM 49
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMAR I
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US-10-264-237-2068	US-09-978-360A-746	US-09-903-190-90	US-09-984-271-116	US-09-984-276-116	US-09-866-050A-313	US-10-143-090-187	US-10-059-395-187	US-09-983-966-187	US-09-966-262-187	US-09-984-271-180	US-09-984-276-180	US-09-984-245-187	ID
Sequence 2068, Ap	Sequence 746, App	Sequence 90, Appl	Sequence 116, App	Sequence 116, App	Sequence 313, App	Sequence 187, App	187,	Sequence 187, App	Sequence 187, App	Sequence 180, App		Sequence 187, App	Description

ALIGNMENTS

ON		
PRIOR APPLICATION NUMBER: US 60/048,099	PRI	
FILING DATE: 1997-05-30	PRI	
APPLICATION N	PRI	
FILING DATE: 1997-05-30	PRI	
PRIOR FILING DATE: 1997-05-30	PRI	
APPLICATION 1	PRI	
FILING DATE: 1997-05-30	PRI	
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FILING DATE: 1997-03-21	PRI	
APPLICATION NUMBER: US	PRI	
FILING DATE: 1997-03-21	PRI	
APPLICATION NUMBER: US	PRI	
FILING DATE: 1997-03-21	PRI	
APPLICATION NUMBER: US	PRI	
FILING DATE: 1997-03-21	PRI	
APPLICATION NUMBER: US	PRI	
FILING DATE: 1998-03-19	PRI	
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FILING DATE: 1998-09	PRI	
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REFERENCE: PZ004P1	FII	
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) ORGANISM: Homo sapiens US-09-984-276-180
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/984,276
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR TILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,925
PRIOR APPLICATION NUMBER: 60/092,926
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
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Best Local S
Matches 49
        Matches
                                          Query Match
                                                                                                                                                             SEQ ID NO 180
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71
FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 180, Appropriate Publication No.
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 187
                                                                                                                      LENGTH: 49
TYPE: PRT
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TYPE: PRT
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                      Local Similarity
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APPLICATION NUMBER: US 60/054,804
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APPLICATION NUMBER: US 60/048,351
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,096
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,069
FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,186
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o. US20030017500A1
      Conservative
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100.0%; Score 260; DB 10; 100.0%; Pred. No. 4.5e-27; tive 0; Mismatches 0;
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Pred. No. 4.5e-27;
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US-09-984-271-180
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US-09-984-271-180
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APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
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PRIOR
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                                                                                                                                                                      PRIOR
                                                                                                                                                                                             PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
                        PRIOR
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TYPE: PRT
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SOFTWARE: PatentIn Ver. 2
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PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
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PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/92,921
PRIOR FILING DATE: 1998-07-15
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CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
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TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                              OR APPLICATION NUMBER: PCT/US98/05311
OR FILING DATE: 1998-03-19
OR APPLICATION NUMBER: US 60/041,277
OR FILING DATE: 1997-03-21
OR APPLICATION NUMBER: US 60/042,344
OR FILING DATE: 1997-03-21
OR APPLICATION NUMBER: US 60/041,276
OR FILING DATE: 1997-03-21
OR APPLICATION NUMBER: US 60/041,281
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             APPLICATION NUMBER: US 60/048,350
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,188
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,135
                                                                                                                          APPLICATION NUMBER: US 60/048,094 FILING DATE: 1997-05-30
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o. US20030050461A1
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5. US20030040088A1
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1997-05-30
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Pred. No. 4.5e-27;
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CURRENT APPLICATION NUMBER: US/09/983,966
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR PELLING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILLING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILLING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR PILLING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR APPLICATION NUMBER: US 60/048,094
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Matches
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Best Local Similarity
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SOPTWARE: PatentIn Ver. 2
SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/060,862
FILING DATE: 1997-10-02
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APPLICATION NUMBER: US 60/054,804
FILING DATE: 1997-08-05
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TILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,160
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,351
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APPLICATION NUMBER: US 60/048,095
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,131
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,069
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PILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,352
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,187
PTI.ING DATE: 1997-05-30
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APPLICATION NUMBER: US
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5. US20030060619A1
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100.0%; Pred. No. 4.5e-27;
tive 0; Mismatches 0;
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US-10-059-395-187; Sequence 187; A)
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PRIOR APPLICATION NUMBER: US/09/966,262
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US/09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR APPLICATION NUMBER: US 60/042,344
                                                                                                                                                                                                                                                                                                        Publication No. US20 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 187
LENGTH: 49
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Best Local
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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PEZ004P1
CURRENT APPLICATION NUMBER: US/10/059,395
CURRENT FILING DATE: 2002-01-31
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OR APPLICATION NUMBER: US 60/050,937

OR FILING DATE: 1997-05-30

OR APPLICATION NUMBER: US 60/048,187

OR FILING DATE: 1997-05-30

OR APPLICATION NUMBER: US 60/048,099

OR APPLICATION NUMBER: US 60/048,099

OR FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,154
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,096
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APPLICATION NUMBER: US 60/048,135
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o. US20030018180A1
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1997-05-30
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FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,276
FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,281
FILING DATE: 1997-03-21

APPLICATION NUMBER: US 60/048,094 FILING DATE: 1997-05-30

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US-10-143-090-187
Sequence 187, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
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Best Local
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
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APPLICATION NUMBER: US 60/048,096
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,355
FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,188
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,135
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APPLICATION NUMBER: US 60/048,095
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,131
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APPLICATION NUMBER: US 60/048,099
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/050,937
FILING DATE: 1997-05-30
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Similarity 100.0%;
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Pred. No. 4.5e-27;
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SOFTWARE: PatentIn Ver. SEQ ID NO 116 LENGTH: 71

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APPLICANT: Murison, James G.

APPLICANT: Kumble, Krishanand D.

APPLICANT: Kumble, Krishanand D.

TITLE OF INVENTION: Compositions Isolated Fr.

TITLE OF INVENTION: and Methods for Their Us.

FILE REFERENCE: 11000.11011c4U

CURRENT APPLICATION NUMBER: US/09/866,050A

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 725

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 313

LENGTH: 70

TYPE: PRT

ORGANTOT:
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          CURRENT APPLICATION NUMBER: US/09/984,276
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,925
PRIOR APPLICATION NUMBER: 60/092,926
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
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NUMBER OF SEQ ID NOS: 343
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               Sequence 116, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthe
                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 71
FILE REFERENCE: PZ030P1
NUMBER OF SEQ ID NOS: 267
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TYPE: PRT
ORGANISM: Homo sapiens
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ilarity 100.0%;
Conservative 0
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Pred. No. 4.5e-27;
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Pred. No. 6.5e-27;
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US-09-903-190-90
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; PEATURE;
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals stop translation
US-09-984-271-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR PFLING DATE: 2000-01-13
PRIOR PFLING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR PILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,925
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-07-15
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; LOCATION: (71)
; OTHER INFORMATION: Xaa equals stop translation
US-09-984-276-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-984-271-116
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                                                                                                                                                                                                                                              Sequence 90, Application US/09903190 Publication No. US20030162176A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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                                                               FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/903,190
CURRENT FILING DATE: 2001-07-11
                                                                                                                               APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                     NT FILING DATE: 2001-07-11
APPLICATION NUMBER: US/09/247,155A
FILING DATE: 1999-02-09
APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNILGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM 49
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b. US20030040088A1
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Pred. No. 6.6e-27;
); Mismatches 0;
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Pred. No. 6.6e-27;
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                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR FILING DATE: 1998-12-17
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
PRIOR PRILING DATE: EARLIER FILING DATE: 1998-04-13
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
                                                                                                                                                       SOFTWARE: Patent.pm
SEQ ID NO 746
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APPLICANT: Cluse1, Catherine
TITLE OP INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/06,957
PRIOR FILING DATE: 1997-12-17
PRIOR PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
                                                                                                                                                                                                          Remaining Prior Application NUMBER OF SEQ ID NOS: 810
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ORGANISM: Homo sapiens
NAME/KEY: SIGNAL LOCATION: -71..-1
                                                     ORGANISM: Homo sapiens FEATURE:
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NAME/KEY: SIGNAL
                                                                                                       TYPE: PRT
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Local Similarity 100.0%;
es 49; Conservation
                                                                                                                                                                                                                                                       FILING DATE: 1999-02-09
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/247,155
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Pred. No. 1e-
0; Mismatches
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-09-978-360A-746

Query Match Best Local Similarity

100.0%;

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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: P07/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1413
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RESULT 15
                                                                                                                                                                                             ; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-925-301-1413
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TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
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US-10-264-237-2068
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1413, Application US/09925301
Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2068
LENGTH: 106
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2068, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Local Similarity 100.0%; Pred. No. 1e-26;
les 49; Conservative 0; Mismatches 0;
                                                     43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
                                                                                                                          49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37
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                                               MNILGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM 91
                                                                                    MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKOMMSSFM 49
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                                                                                                                                         100.0%; Score 260; DB 9; Length 112; 100.0%; Pred. No. 1.1e-26;
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Pred. No. 1e-26;
); Mismatches 0; Indels 0
                                                                                                                          Mismatches
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US-10-276-774-2348

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PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SEQ ID NO 2348
LENGTH: 132
                                                                                            Query Match 100.0%; Score 260; DB 15; Best Local Similarity 100.0%; Pred. No. 1.3e-26; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2348, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245A
FILE REFERENCE: 21272-030
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                TYPE: PRT
  63
                              1 MNILGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM 49
MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US20040053245A1el Nucleic Acids and Polypeptides
                                                                                              Indels
                                                                                                                                            Length 132;
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Search completed: March Job time : 94 secs 6, 2005, 08:19:20

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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260
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4: pir4:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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ALIGNMENTS

hypothetical protein K10B2.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #to C;Accession: T16603 R;Miller, N.

20-Sep-1999 #text_change 09-Jul-2004

T16603

A;Description: The sequence A;Reference number: Z18545 A;Accession: T16603

from GB/EMBL/DDBJ

submitted to the EMBL Data Library, June 1995 $A_{\rm F}$ Description: The sequence of C. elegans cos

cosmid K10B2

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A;Map position: 5
A;Introns: 53/3; 87/2
A;Note: F13G24.160
C;Superfamily: Caenorhabditis elegans hypothetical protein K10B2.4
                                                                                                                                                                                                                                                                R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23009
A;Accession: T45621
                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <BEV>
                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F13G24.160 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45621
                                                                                                                                                   A;Cross-references: UNIPROT:Q9SD88; EMBL:AL133421
A;Experimental source: cultivar Columbia; BAC clone F13G24
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C;Superfamily: Caenorhabditis elegans hypothetical protein K10B2.4
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A;Experimental source: strain Bristol N2
                                                                                                                                   ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.1%;
Best Local Similarity 69.4%;
Matches 34; Conservative 12
Query Match
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Pred. No. 4.3e-20;
.2; Mismatches 3;
Score 73.5;
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 113;
Length 107;
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; aneen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wenter, J.C.; Davis, R.W.

A;Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9C9J5; GB:AE005173; NID:g6642680; PIDN:AAF20260.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-971 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F14G6.23 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: E96794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Recession: F64484
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C;Superfamily: aspartate transamina
C;Keywords: aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-432 <BUL>
A;Cross-references: UNIPROT:Q58874; GB:U67588; GB:L77117; NID:g1592111; PID:g1592118; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable transaminase (EC 2.6.1.-) MJ1479 [similarity] - Methanococcus jannaschii N;Alternate names: alanine aminotransferase 2
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                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
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                                                                                                                                               Query Match
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Best Local Similarity 29.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                  position:
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                                                                                                                                                                                                                            F14G6.23
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                                                                                                              Similarity
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NLLGMIFSNCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKOMMSS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLGMIFSMCGLMLK-----LKW----CAWVAVYCSFISFANSRSSEDTKQMMSS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AVILGVSGVMFRYKICSWLAIIFCAQSLANMRNLENDLKQISMAMM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSE-DTKOMMSSFM 49
                                                                                       Conservative
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                                                                                                           22.7%;
                                                                                 2; Mismatches
                                                                                                        Score 59; DB
Pred. No. 7.7;
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                                                                              24; Indels
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                                                                                                                              Length 971
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                                                                                 G90266
na(+)/H(+) antiporter [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90266
C;Accession: G90266
        R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                RESULT
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8

Sulfolobus solfataricus complete genome

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A;Gene: SPAC18B11.08c
A;Map position: 1L
A;Introns: 25/1; 44/2; 74/2; 87/1
                                                                                                                                                                                                                                                                                                  A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z50728; NID:g929886; PID:g929894; PIDN:CAA90596.1; GSPDB:GN00066 A;Experimental source: strain 972h-; cosmid c18B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, August 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SPAC18B11.08c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 13-Jan-196 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000 C;Accession: T37906; S59846
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S59846
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                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z21753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CC1930
C;Superfamily: hypothetical protein HI1555
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A;Molecule type: DNA
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                                                                                                           Matches
                                                                                                                                          Query Match
Best Local :
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                                       1 MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSS 38
                                                                                                             12;
LSLVSTATCMAALFLRFKLIAWVAFILTFSNLLNANTS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRS
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                                                                                                        Conservative
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                                                                                                                              21.9%;
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                                                                                                           в
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                                                                                                     Score 57; DB 2; Length 103; Pred. No. 1.9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fission yeast (Schizosaccharomyces pombe)
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probable membrane protein YDR384c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D9481.20
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S61179; S69668
C;Accession: S61179; S69668
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of S. cerevisiae cosmid 9481.
A;Reference number: S61159
A;Molecule type: DNA
A;Residues: 1-275 cDIN
A;Residues: 1-275 cDIN
A;Residues: 1-275 cDIN
                                                                                                     A;Cross-references: UNIPROT:Q12359; EMBL:U283:
A;Experimental source: strain S288C (AB972)
R;Dietrich, F.S.
R;Dietrich, F.S.
A;Description: The EMBL Data Library, July 1995
A;Description: The sequence of S. cerevisiae of A;Reference number: S69865
A;Recession: S69668
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S61179
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A;Accession: T26392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-489 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y105C5B.f - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T26382 R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:Y105C5B.f
A;Introns: 58/3; 79/3; 114/1; 148/3; 176/2; 233/3;
C;Superfamily: Caenorhabditis elegans hypothetical
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                    A;Cross-references: EMBL:U32274; NID:g927313; PIDN:AAB64826.1; PID:g927317; MIPS:YDR3840
C;Genetics:
                                                               A; Molecule type: DNA
A; Residues: 1-275 < DIE>
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C;Genetics:
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A; Residues: 1-391 <KUR>
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A;Status: preliminary
A;Cross-references: SGD:S0002792
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Matches
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9; Conserv
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Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                 EMBL:U28373; NID:g849184; PIDN:AAB64820.1; PID:g8497 (AB972)
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protein Y105C5B.
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                                                                                                                                                    9461,
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A;Cross-references cultivar Columbia A;Experimental source: cultivar Columbia R;Kalicki, J; Gibson, A. submitted to the EMBL Data Library, August submitted to the sequence of A, thaliana
                                                                                                                                                                                                                                                                                           Martienssen, R.; McCombie, W. submitted to the EMBL Data Library, May 1997 A;Description: The sequence of the Arabidopsis A;Reference number: Z14346 A;Accession: T01520
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T10M13.18 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear Cress) (Species: Arabidopsis thaliana (Mouse-ear Cress) (C;Date: 19-Feb-1999 #Bequence_revision 19-Feb-1999 #Lext_change 09-Jul-2004 (C;Accession: T01520; T01431 (C;Accession: T01520; T01431 (C;Accession: R), MCCambic W.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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                                                A; Reference number: Z14324
A; Accession: T01431
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-659 < JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: C70803
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Nature 393, 537-544, 1998
A;Status: translated from A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4R
                                                                                                                                                                                               A;Cross-references: UNIPROT:004257; EMBL:AF001308; NID:g2104523; PID:g3912924
                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: 069741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-511 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Rv3877 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004; Date: 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMIFSMCGLMLKL---KWCAW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFSMCGLMLKLKWCAWVAVYCSFISFANS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                            GB/EMBL/DDBJ
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262
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hypothetical protein C34C6.2 - Caenorhabditis elegans C, Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_C; Accession: T19705 R; Percy, C.
Submitted to the EMBL Data Library, October 1995 A; Reference number: Z19167 A; Residues: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-821 < WILD
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                                                                                                                                                  A;Map position: 2
A;Introns: 50/3; 79/2; 139/1; 301/3; 334/1; 387/1; 469/3; 614/1; C;Superfamily: Caenorhabditis elegans hypothetical protein C34C6.
                                                                                                                                                                                                                                        A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q18423; A;Experimental source: clone C34C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Protein Sequence
A;Reference number: Z17528
A;Accession: T12487
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-520 <OTT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp566K0247.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999 C;Accession: T12487 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF075597; NID:g3298610; PID:g3377807
A;Experimental source: cultivar Columbia
C;Genetics:
C;Genetion: 45
A;Nap position: 45
A;Note: T10M13.18; T2H3.14
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A;Experimental source: fetal kidney;
                                                                         Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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113
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                                     17 LKWCAWVAVYCSFISFANSRSSEDTK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LIGMIFSMCGLMLKLKWCAWVAVYCSFISFAN----SRSSEDT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NILGMIFSMCGL-MIKIKWCAWVAVYC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 21.2%;
Similarity 40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%;
Similarity 34.9%;
LKWCMQVLNHSLTLSFATSREYETLK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPGVLDNICGNKIHSKWACWTPV--TNIELCNNQRASTSSGDT
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                                                                                              20.8%;
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                                                                                              Score 54; DB
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB
Pred. No. 21;
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                                                                             Mismatches
                                                                                                                                                                                                                                                                                EMBL: Z66494; PIDN: CAA91257.1; GSPDB: GN00020; CESP: C3
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                                                                                                                 DB 2;
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                                                                             12; Indels
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                                                                                                                 Length 821;
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RESULT 14

Search completed: March

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Riffleologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 815-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Kowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wuther, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-217 <GLA>
A;Cross-references: UNIPROT:Q8Y6R1; GB:NC_003210; PIDN:CAC99701.1; PID:g16411059; GSPDB:CA;Cross-references: UNIPROT:Q8Y6R1; GB:NC_003210; PIDN:CAC99701.1; PID:g16411059; GSPDB:C;Genetics:
                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9C6S5; GB:AE005172; NID:g11136719; PIDN:AAG31300.1; GSPDB:GNC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable amino acid permease [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
D86442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1277
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C;Species: Listeria monocytogenes
C;Species: 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1277
C;Accession: AG1279
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
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A; Residues: 1-495 <STO>
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                                                                                                              Matches
                                                                                                                                        Best
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                                                                                                                                                                                                                         position: 1
                                                                                                                                        Local
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359
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17; Conserv
                                                       3 LLGMIFSMCGLMLKLKWCAWVAV-----YC----SFISFANSR 36
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNLLGMIFSMCGLMLKLKWCA-----WVAVYCSFISFANSRSSEDTKQMMSSFM 49
IGLLGFIFFMTGVMTGAKWIQRFDHYWNSVIRVGIT-----DTKTTVISYL 56
                                                                                                              Conservative
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Voss, H.; Wehland,
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Match
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1: uniprot_sprot:*
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Gapop 10.0 ,
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9BVI3
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45	44	43	42	41	40	39	38	37	36	35	34	33	32
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ALIGNMENTS

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SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703; Lai CH., Chou CY., Ch'ang LY., Liu CS., Lin WC.; "Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics."; Genome Res. 10:703-713(2000). [2] SEQUENCE FROM N.A.		1 MNLIGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM 49	Query Match 100.0%; Score 260; DB 2; Length 104; Best Local Similarity 100.0%; Pred. No. 8.4e-27; Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0	SEQUENCE FROM N.A. TISSUB-Eye; Strausberg R.; Strausberg R.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; BC001192; AAH01192.1; InterPro; IRR05351; UPF0139. Pfam; PF03669; UPF0139; 1. ProDom; PD073147; UPF0139; 1. NON TER 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	9BVI3; L-JUN-2001 (L-JUN-2001 (L-JUN-2003 (13 Q9BVI3 PRELIMINARY; PRT; 104 AA.

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RESULT 4
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ID Q6ZW
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Lee H.Y., Cui X.S., Shin M.I
Submitted (FEB-2004) to the
EMBL; AY553921; AAS76542.1;
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05-JUL-2004
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05-JUL-2004
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ProDom; PD073147; UPF0139; 1.
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Mammalia; Eutheria;
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EMBL; AF079861; AAD44493.1; -.
EMBL; AF059620; AAD43119.1; -.
InterPro; IPR005351; UPF0139.
Pffam; PF03669; UPF0139; 1.
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Mao Y.M., Xie Y., Zhou Z
Submitted (APR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Song H., Peng Y., Dai M., Huang Q., Mao Y., Zhang Q., Ma
Luo M., Chen J., Hu R.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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Song H., Peng Y., Dai M.,
Luo M., Chen J., Hu R.;
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106 AA;
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                                                                                                                                                                                                                                                                                                                0
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Last annotation updat
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                                                                                                                                                                                                                                                                                                            Score 260; D
Pred. No. 8.6
); Mismatches
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; 7D2BDDAF9279071B
                              PRT;
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Pred. No. 8.6e-27;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0CB2D4249AD258E7 CRC64;
                                                                                                                                                                                                                                                                                                                                          260; DB 2;
No. 8.6e-27;
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Coutstation -
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STRAIN=578L/GJ; TISSUE-Liver;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Alakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno I
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno I
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno I
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai J
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki Y.
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino
Muramatsu M., Hayashizaki Y.,
Shinataki Y.,
Shinataki Y., Tanaka T
                                                                                                                                                                                                                                                                                                         MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegani T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Wataki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; denome Res. 10:1757-1771(2000)
SEQUENCE
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUB-Liver;

MEDLINE=2049974; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muraninci N., Hayashizaki Y., Wormalization and subtraction of cap-trapper-selected cD prepare full-length cDNA libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=20530913; PubMed=11076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver;
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STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=21085660; PubMed=11217851;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-JUL-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 13 days embryo liver cDNA, RIKEN full-length e
library, clone:2510002P07 product:PROTEIN CGI-140 (PROTEIN
homolog (CDNA sequence BC056474).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=BC056474;
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                             EMBL/GenBank/DDBJ databases
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOI=10.1016/S0076-6879(99)03004-9;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P.,
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Best Local S
Matches 49
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& Strausborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

& Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,

& Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

& Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Foshiyuki S., Carninci P., Prange C.,

& Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

& Brownstein M.J., Wallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

& Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

& Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,

& Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,

& Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

& Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

& Pahey J., Helton E., Ketteman M., Madan A., Gotrigues S., Sanchez A.,

& Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

& Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

& Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

& Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

& Jores G. J. Marra M.A.
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Q6DKM8;
25-OCT-2004
25-OCT-2004
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Alek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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ProDom; PD073147; UPF0139; 1.
SEQUENCE 106 AA; 12068 MW;
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Submitted (AUG
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Name=MGC82186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
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28,
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Last sequence update)
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Pred. No. 8.6e-27;
; Mismatches 0;
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PRESENTATION OF THE PRESEN
                  RA Strausberg R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsiah F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
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Best Local S
Matches 48
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGC81480 protein.
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Pfam; PF03669; UPF0139; 1.
ProDom; PD073147; UPF0139; 1.
SEQUENCE 106 AA; 11885 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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.J., Marra M.A.;
tion and initial
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   analysis
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Last annotation updat
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than 15,000 full-length humar
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RC STRAIN-Wild-type; TISSUE=Eye;
RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Bonaldo M.F., Carninci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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Best Local Similarity
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Klein S., Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ
EMBL; BC068836; AAH88836.1; -.
InterPro; IPR005351; UPF0139.
Pfam; PF03669; UPF0139; 1.
ProDom; PD073147; UPF0139; 1.
PRODOM; PD073147; UPF0139; 1.
                SEQUENCE FROM N.A. STRAIN-Wild-type;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6PC46;
 Strausberg
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:73111.
ORFNames=zgc:73111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish)
Bukaryota, Metazoa, Chordata,
Actinopterygii, Neopterygii, T
                                                                                                  "Generation and initial analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyprinidae; Dani
NCBI_TaxID=7955;
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Klein S.L., Strausberg R.L., Wagner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                  .J., Marra
                                                                 cDNA sequences.";
l. Acad. Sci. U.S.A.
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                TISSUE=Eye
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; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniform
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Pred. No. 1.2e-26;
                                                                 99:16899-16903 (2002)
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                                                                                                  of more than 15,000
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r L., Pontius J., Clifton S.W.,
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RESULT 9
U139 MANSE
ID 'U139 M
AC Q9U516
DT 16-OCT
DT 16-OCT
DT 29-MAR
DE HYPOTH
OS MANDUC
OC Eukary
OC Neopte
OC Sphing
OX NCELT
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
RA ROBERT
                                                     Q9USI6;
1 Q9USI6;
1 GOCT-2001 (Rel. 40, Created)
1 16-OCT-2001 (Rel. 40, Last sequence update)
1 16-OCT-2001 (Rel. 43, Last annotation update)
1 29-MAR-2004 (Rel. 43, Last annotation update)
2 Hypothetical UPF0139 protein pMsmaA27.
2 Manduca sexta (Tobacco hawkmoth) (Tobacco hornwoods Eukaryota; Metazoa; Arthropoda; Hexapoda; Inseco CC Neoptera; Endopterygota; Lepidoptera; Glossata; Sphingidae; Sphinginae; Manduca.
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Q7QIP7
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Best Local
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Best Local
 MEDLINE=20099029; PubMed=1
                          SEQUENCE FROM N.A.
TISSUE=Antenna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7QIP7;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AAAB01008807; EAA04290.1; -.
InterPro; IPR005351; UPF0139.
Pfam; PF03669; UPF0139; 1.
                                                                                                                                                                                                      U139 MANSE
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD073147; UPF0139; 1. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=agCG54409; ORFNames=ENSANGG00000012639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgCP3421 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae str.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC059477; AAH59477.1; -. ZFIN; ZDB-GENE-040426-1674; zgc:73111.
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                                                                                                                                                                                                                                                                                 1 MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
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48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            130 AA;
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106 AA; 12202 MW;
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                                                                                                                                                                                                   STANDARD;
            PubMed=10620045;
                                                                                                                                                                                                                                                                                                                                                                          14648 MW;
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 Sears C.R.,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                       Score 221; DB 2;
Pred. No. 1.7e-21;
7; Mismatches 3
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                                                                                       acco hornworm).
oda; Insecta; Pterygota;
Glossata; Ditrysia; Sph
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E.Z., Walden K.K.O.,
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RESULT 10
QAXIW
OGXIW7
QAXIW
AC QAXIW
DT 05-JU
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RESULT 11
U139 DROME
ID U139 DROME
AC Q9VRJ8;
DT 16-OCT-2001
DT 16-OCT-2001
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 38
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6XIW7
Q6XIW7;
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003; Domazet-Loso T., Tautz D.; Pan evolutionary analysis of orphan genes in Drosophila."; Genome Res. 13:2213-2219 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila yakuba (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to Drosophila melanogaster CG10674 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03669; UPF0139; 1. ProDom; PD073147; UPF0139; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY231712; AAR09735.1; - InterPro; IPR005351; UPF0139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera; Endopterygota; Diptera; Brach
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP03669; UPP0139; 1.
Probom; PD073147; UPP0139; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 77 93
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                      38;
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                                                                                                                                                                                                                                                                                                                                                 Similarity
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B.
                                                                                                                                                                                                                                      MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFN 49
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                                                                                                                                                                                                                                                                                                                                                                                                                            102 AA;
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(Rel. 40, Creat (Rel. 40, Last
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                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         102
11397 MW;
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                                                                                                                                                                                                                                                                                                                                               83.5%;
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                                                                                                                                                                                                                                                                                                                                               Score 217; DB 2;
Pred. No. 4.6e-21;
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                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            B13EE02BD0915D79 CRC64;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Holtards S., Ashburner M., Galle R.F.,
RA George R.A., Lewis S.E., Hichards S., Ashburner M., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Clampe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlis W.R., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bertis K.C., Blasem D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milahina N.S., Pan S., Pelebb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Slapson M., Skupski M.P., Smith T.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhao Q.A.,
Who Sheng E.M., Roodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
"The genome sequence of Drosophila melanogaster.",
RI Science 287:2185-2195 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12535772;
Misra S., Crosby M., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.I
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                 systematic review. Genome Biol. 3:RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2005 (Rel. 46, Last annotation update)
Hypothetical UPF0139 protein CG10674.
ORFNames=CG10674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENOME REANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            'Annotation of the
                                                                                                                                                                                                                                                                ome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
SIMILARITY: Belongs to the UPF0139 (CGI-140) family.
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                            It is produced through a collaboration
                                            There are no restrictions of as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                 euchromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muscomorpha;
                                                                                                                                         and the EMBL
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                                                                                                                                             outstation
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RESULT 13
Q8LKT8
ID Q8LKT
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U139_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                            Query Match
Best Local
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Best Local S
Matches 38
         Q8LKT8
                                                                                                                                                                                                                                                                                                                    Fronom; PD073147; UPF0139; 1.

Hypothetical protein; Transmembrane.

TRANSMEM 81 97

SEQUERATE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    WormBase; WBGene00019607; K10B2.4. WormPep; K10B2.4; CB02011. InterPro; IPR005351; UPF0139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U139 CAEEL
Q09993;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U28730; AAA68261.1; -. PIR; T16603; T16603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform investigating biology.", Science 282:2012-2018 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last amoutation update)
Hypothetical UPF0139 protein K10B2.4 in chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=K10B2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03669; UPF0139; 1.
ProDom; PD073147; UPF0139; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 80 96 Potenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IntAct; Q9VRJ8; -.
FlyBase; FBgn0035592;
InterPro; IPR005351; UniterPro; UniterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003567; AAF50797.1; -.
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                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the UPF0139 (CGI-140) family.
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                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
38; Conserv
                                                                                                            MMLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA;
    PRELIMINARY;
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA;
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                                                                                                                                                                                                                                                                                                          12764 MW;
                                                                                                                                                                                                                                  78.1%;
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                                                                                                                                                                                                            12;
                                                                                                                                                                                                  Pred. No. 3./c
2; Mismatches
                                                                                                                                                                                                                             Score 203; DB 1;
Pred. No. 3.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 217; Db .,
Pred. No. 4.8e-21;
                                                                                                                                                                                                                                                                                                                                Potential
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
                                                                                                                                                                                                                                                                                                  0FEED534A710DD50 CRC64;
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153
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B
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                                                                                                                                                                                                                                                    Length 113;
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                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                       Gaps
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RESULT QUAUTIC PARTIES AC QUAUTIC QUAU
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                           Matches
                                                           Query Match
Best Local
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                                                                                                                                                                               ProDom; Proposed Prop
                                                                                                                                                                                                                                                                                                                                                                   Gramene; Q9AUU6;
InterPro; IPR005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAke
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AUU6;
01-JUN-2001 (TrEWBLrel. 17, Created)
01-JUN-2001 (TrEWBLrel. 17, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation updat
Hypothetical protein OSJNBa0040E01.6.
                                                                                                                                                                                                                                                                  Pfam; PF03669; UPF0139; 1. ProDom; PD073147; UPF0139; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC079887; AAK16184.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AUU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (T
Hypothetical p
Name=170F8.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8LKT8;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF503433; AAM47587.1; ...
InterPro; IPR005351; UPF0139.
Pfam; PF03669; UPF0139; 1.
ProDom; PD073147; UPF0139; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Different types and rates of genome evolution sequence analysis of orthologous segments from Genetics 162:1389-1400(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 153 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22341483; PubMed=12454082;
Ramakrishna W., Dubcovsky J., Park Y.J.,
SanMiguel P., Bennetzen J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TaxID=39947;
                  l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR005351; UPF0139.
                  Conservative
                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TIRMBLrel. 22, Created)
(TIRMBLrel. 22, Last sequence up
(TIRMBLrel. 24, Last annotation
protein 170F8.12.
                                                                                                                                                                                   9961 MW;
                                                       33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16498 MW; 0A59856FE6FC4CE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.8%; Score 90.5; 1
38.3%; Pred. No. 0.00
tive 12; Mismatches
             12;
Score 86.5; DI
Pred. No. 0.001
12; Mismatches
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STRAIN-AX4;

MEDLINE-22092622; PubMed=12097910; DOI=10.1038/nature00847;

MEDLINE-22092622; PubMed=12097910; DOI=10.1038/nature00847;

Gloockner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,

Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,

Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;

"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";

Nature 418:79-85(2002).
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116960; AAO53170.1; -
InterPro; IPR005351; UPF0139.
Pfam; PF03669; UPF0139; 1.
ProDom; PD073147; UPF0139; 1.
ProDom; PD073147; UPF0139; 1.
Hypothetical protein.
SEQUENCE 98 AA; 11011 MW; 1D44628B4806ABDE CRC64;
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086H65;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Dictyostelium discoideum (Slime mold).
Enkaryota, Mycetozoa; Dictyosteliida; Dictyostelium.
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Maximum DB seq length: 2000000000
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ORGANISM
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VERSION
KEYWORDS
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AL138904/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 118782 bases at least Q40
Consensus quality: 121247 bases at least Q30
Consensus quality: 122835 bases at least Q20
Insert size: 125380; sum-of-contigs
Insert size: 135380; sum-of-contigs
Quality coverage: 3.66x in Q20 bases; sum-of-contigs Quality
Coverage: 3.42x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: dJ932F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 27, 2000 this sequence version replaced gi:9796269.
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AL138904.4 GI:9931278
HTG; HTGS_PHASE1; HTGS_HOME
HOMO sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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22625:
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36189:
36189:
36189:
50092:
50192:
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13996:
14096:
17758:
99: contig of 3279 bp in length
99: gap of 100 bp
86: contig of 10617 bp in length
86: gap of 100 bp
88: contig of 3662 bp in length
89: contig of 4767 bp in length
15: contig of 4767 bp in length
15: gap of 100 bp
10: contig of 7527 bp in length
10: gap of 100 bp
10: contig of 6276 bp in length
10: gap of 100 bp
10: gap of 100 bp
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10: contig of 5948 bp in length
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76 TGCTCTTACTGTTGAAAACATTATTTGTTACATTTTGGTCAACTAATCTTTCAATAACTT	Qy 16 TTAATGTATAAAATATTTCTATAATGAATTTTAATGGGAATTAGAGCATCATAGAAAAA 75	Query Match 97.5%; Score 1011.6; DB 2; Length 126780; Best Local Similarity 99.1%; Pred. No. 3.5e-187; Matches 1011; Conservative 5; Mismatches 4; Indels 0; Gaps 0;		feature	feature :	/note="a	notes"a		/note="assembly_fragment:00987	/notes assembly tragment: votet misc_feature fragment chain:2" misc_feature 5019356140	misc_feature 43817. 50092	tragment_chain:2" misc_feature	misc_feature 3324136089 /note="assembly_fragment:01055	0	reature		/noce="assembly iragment:00030 fragment chain:I" misc feature 14097. 1758	misc_feature 3380. 13996	misc_feature 1.3079	/ Call Call Call Call Call Call Call Cal		119442 126780: contig Location/Qualifies 1126780	116755 119341: contig of 2587 bp in 119342 119441: gap of 100 bp	100170: gap of 116654: contig	59541 59640: gap of 100 bp 59641 82808: contig of 23168 bp in 82809 82908: gap of 100 bp	56240: gap of 59540: contic
SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Db 63800 ATTGCACTCCAGCCTGGGCAACACAGTGAGACTCTTGTCTCAAAAAAAA	976 ATTGCACTCCAGCCTGGGCAACACAGTGAGACTCTTGTCTCAAAAAAAA		Qy 916 ACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCC 975	Db 63920 GTCTCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCT 63861	Qy 856 GTCTCTACTAAAATACAAAAATTAGACAGGGGTGGGTGGCACACATCTGTAATTCCAGCT 915	Oy 796 GCAGGTGGATCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAACGTT 855 Db 63980 GCAGGTGGATCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAACGTT 63921	64040 TAGTCCAGGGCTGGGCGCGATAGCTGATGCCTGTAATCCCAGTACTTTGCGGGGCCCAG	Qy 736 TAGTCCAGGGGCTGGGCGGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGCCGAG 795	Db 64100 TTACCTGACAAAATCTTAGCCAGTTCTTCATTTTCGTTTTGAGATGAAGATACTTAGTTT 64041	64160 GAGTATGACTACAAAACAGGAAAAAAAAAAAAAAAAAAA	616 GAGTATGACTACAAAACAGGAAAAAATAAACAGATTTCGTTTGTGGCTTTTGCTAAATTG 6	Db 64220 TCCATGCAAAGTTAAAATTCTTCAGCCTTTAATTTTTTTATTAATATATAT	64280 AGTCTTCAAAGGTATTACAATTATAAAAACCTTTGGTTTTTATTCTTTGTGAATAAAACCGTTTTTT 6	Qy 496 AGTCTTCAAGGKATTACATTATAAAAACCTTGGKTTTTATTCTTGTGAATAMCCGTTTTT 555	Db 64340 CTAAAATTATAGTTGTTAAATACGCTTTTGTAAATAGTTGTGTTATGGTCATTATCACCA 64281	7.2.6 OFFICE THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE	Qy 376 GTAGGCAAACTTATATAATCTGTCAACTCCATTAGTGTCATAGTCAGACTCATCCCCATG 435	Qy 316 ATGATTTGACGTTTGTGWAAATATTTTCCCTGGACTTTATTTTAGATGAGATCTACAGT 375		256 CAAAACCTTGTTAGTTTTTTAGGGTATAGTCACATTTTATAAATGTGCGGTATATTTATAC 3	Qy 196 AGCATGAAAATAACATATCTAATATTTTGTGACTATCTTATTAGGAAAATCAGAGAATTT 255	Qy 136 TTAGTAACTATAATGTTAAGTTGTACCAGTGGCAGTCTTATATAGTAAATGGCAGCTGAC 195	TGCTCTTACTGTTGAAAACATTATTTGTTACATTTTGGTCAACTAATCTTTCAATAACTT

		REFERENCE AUTHORS TITLE JOURNAL REFERENCE TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS
quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Sequence validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. BglII BglII	Center University of Washington Genome Center Code: UMCC Web site: http://www.genome.washington.edu Drafting Center: SC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 141670) Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D. Direct Submission Unpublished 2 (bases 1 to 141670) Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D. Direct Submission Submitted (195-DEC-2001) Genome Center, University of Washington, Staul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D. Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D. Direct Submission Submitted (23-PEB-2002) Genome Center, University of Washington, Submitted (23-PEB-2002) Genome Center, University of Washington, On Feb 23, 2002 this sequence version replaced gi:17352434.
2571 183 11422 136 4113 2446 1212 6024 4066	4358 453 453 453 453 8754 8754 13263 13263 1302 221 221 3182 8583 2881 2881 2887 2887 3858 2049 1828 728 3103	SeqDerMap
2641 <800 1373 <800 4141 2497 1162 5993 <800 4013	4277	FngrPrnt 8789 <800 <800 1583 10649 <800
456 8747 8747 4056 	4491 743 3989 114808 8390 2696 4219 110947 110947 11478 3621 1683 11017 3136 6377 540 1891	SeqDerMap
456 <800 8747 8822 4056 4039 2370 2478 2370 5021	4491 4481 743 <800 3989 3943 114808 14844 8390 8521 2696 2710 4219 4162 110947 10800 2158 2142 1478 1452 3621 3657 1683 1639 11017 1022 3136 3207 6377 6455 540 <800 1890	SeqDerMap FngrPrnt
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Query Match Boot Local Similarity 99.1%; Score 1011.6; DB 9; Length 141670; Boot Local Similarity 99.1%; Pred. No. 3.5e-187; Matches 1011; Conservative 5; Mismatches 4; Indels 0; Gaps 0; Oy 16 TTAATGTATAAAATATTTCTATATGAATTTAATGGGAATTAGAGCATCATAGAAAAA 75	1339 1373 5115 5021
AL359698 AL359698 AL359698 AL359698 ACCESSION AL359698 AL35968 AL36968 AL36968 AL36968 AL36968 AL36968 AL3696	Qy 496 AGTCTTCAAGGKATTACATTATAAAACCTTTGKTTTATTCTTGTGAATTACCGTTTTT Db 2030 AGTCTTCAAGGTATTACATTATAAAACCTTTGGTTTTTATTCTTGTGAATTACCGTTTTT CO24 S56 TCCATGCAAGGTATTACAATTCTTCAGCCTTTAATTTTTTATTATTATATATA

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                               AGTCTTCAAGGTATTACATTATAAAAACCTTTGGTTTTTTATTCTTGTGAATAACCGTTTTT
AGTCTTCAAGGKATTACATTATAAAAACCTTGGKTTTTATTCTTGTGAATAMCCGTTTTT
                                                                                               CTAAAATTATAGTTGTTAAAATACGCTTTTGTAAATAGTTGTGTTAGGTCATTATCACCA
                                                                                                                    CTAAAATTATAGTTGTKAAAATACGCTTTTGTAAATAGTTGTGTTAGGTCATTATCACCA 495
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/mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="X"
/clone="RP11-55316"
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23922._.31390
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31491. .164500
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99.1%;
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23921: gap of 100 bp
31390: contig of 7469 bp in length
31490: gap of 100 bp
14500: contig of 133010 bp in length
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Pred. No. 3.5e-187;
5; Mismatches 4;
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AL731898/c
LOCUS
DEFINITION
ACCESSION
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                                               Assembly program: XGAP4; version 4.5
Sequencing vector: Ml3; M77815; 54% of reads
Sequencing vector: plasmid; 108752; 45% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-terminator; 0% of reads
Consensus quality: 169292 bases at least Q40
Consensus quality: 169299 bases at least Q20
Consensus quality: 169299 bases at least Q20
Insert size: 169304; sum-of-contigs
Insert size: 114813; 2.3% error; agarose-fp
Quality coverage: 18.08x in Q20 bases; sum-of-contigs
Coverage: 17.90x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 14, 2002 this sequence version replaced gi:20429020.
                                                                                                                                                                                                                                                                                                           Center project name: bA449B11
                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169304)
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HTG; HTGS_PHASE2; HTGS_CANCELLED.
NOTE: This is a 'working draft' sequence. consists of 1 contigs. Gaps between the co
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Homo sapiens chromosome 1 clone RP11-449B11.
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 163304: contig of 169304 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                     GTAGGCAAACTTATATAATCTGTCAACTCCATTAGTGTCATAGTCAGACTCATCCCCATG 435
                                                                                                                                                                                                                                                                                                                                                          CAAAACCTTGTTAGTTTTTAGGGTATAGTCACATTTTATAAATGTGCGGTATATTTATAC
                                                                                                                                                                                                                                                                                                                                                                            CAAAACCTTGTTAGTTTTTAGGGTATAGTCACATTTTATAAATGTGCGGTATATTTATAC 315
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                                               GAGTATGACTACAAAACAGGAAAAAATAAACAGATTTCGTTTGTGGCTTTTGCTAAATTG
                                                                                                                                                               AGTCTTCAAGGKATTACATTATAAAAACCTTGGKTTTTATTCTTGTGAATAMCCGTTTTT
                                                                                                                                                                                                     CTARARTTATAGTTGTTARARTACGCTTTTGTARATAGTTGTGTTAGGTCATTATCACCA
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               TTACCTGACAAAATCTTAGCCAGTTCTTCATTTTCGTTTTTGAGATGAAGATACTTAGTTT
                                                                                                                TGCTCTTACTGTTGAAAACATTATTTGTTACATTTTGGTCAACTAATCTTTCAATAACTT 135
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                                                                        GAGTATGACTACAAAACAGGAAAAATAAACAGATTTCGTTTGTGGCTTTTGCTAAATTG
                                                                                                   TTAGTAACTATAATGTTAAGTTGTACCAGTGGCAGTCTTATATAGTAAA!GGCAGCTGAC 195
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-449B11"
/clone=lib="RPCI-11.2"
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clone_end:T7
vector_side:right"
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Pred. No. 3.5e-187;
5; Mismatches 4;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41322)

Lamerdin, J.E., McCready, P.M., Skowronski, B., Adamson, A.W.,

Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,

Garnes, J., Danganan, L., Poundstone, P., Christensen, M.,

Georgescu, A., Avila, J., Liu, S., Bruce, R., Quan, G., Montgomery, M.,

Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.O. and

Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-JAN-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Map and sequence oriented from centromere to q telomere.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence analysis of a 500 kb ZNF gene family- containing human contig in 1943.4 Unpublished 2 (bases 1 to 41322)
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Homo sapiens
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AC004076
AC004076.1 GI:2822142
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Lamerdin, J.E.
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/note="BLASTN similarity to AC003002 (80114...81544);
match: 1, score: 1.8e-294; database searched: nt; Human
DNA from overlapping chromosome 19-specific cosmids R29515
and R28253, genomic sequence, complete sequence (Homo
sapiens);
complement(10...98)
/rpt_family="MSTC"
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/cell line="5Hl2-B"
/cell line="5Hl2-B"
/clone lib="LL19NC032 R chromosome 19-specific cosmid"
/note="cosmid library constructed at LLNL from flow-sorted
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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/clone="R30217"
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/mpt_family="LINE2"
complement(6952...6980)
/mpt_family="AT_rich"
7067...7364
                                                                                                                                                 overlapping matches:
(11508..11634) predicted exon, program:
grail2exons human_1.3, frame: 2, quality: excellent,
score: 83.000"
12108..12167
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/note="DPS similarity to (U66561) kruppel-related zinc
/niger protein [Homo sapiens] (64. .249).~Other overla
                                                                                                      finger protein [Homo 12861. .12900
                                                                                                                                                                                                                           /note="DPS similarity to (U66561) kruppel-related zinc finger protein [Homo sapiens] (1. .43); 48% identity. Other
                                                                                                                                                                                                                                                                                                                        frame: 1, quality: excellent, score: 90.000" 10469. .10758
     (12973. .15108) predicted exon, program:
                                                                                                                                                                                                                                                                                                                                                                                                                      complement (8649. .9102)
/rpt_family="LINE2"
                                                                                                                note="DPS similarity to (U66561) kruppel-related zinc inger protein [Homo sapiens] (45. .63); 26% identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (7488.
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complement(2735. .2777)
/rpt family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contains LTR3.b1 LTR3 repetitive element; (1. .253); 96%
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/note="DDS similarity to AA229025 nc50c11.sl NCI_CGAP_Pr3
Homo sapiens cDNA clone IMAGE:1011572. Score: 550
Identity: 290/300 (96%)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="AluSg"
Dlement(7488. .7593)
family="MIR"
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. .11576
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complement(22738..22856)
/rpt_family="(GGAA)n"
complement(22871..23168)
                                             complement (22532. .22641)
/rpt_family="L1MA9"
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/rpt_family="MSTC"
complement(21068. .21397)
/rpt_familv="""
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complement(17364. .1765a)
/rpt_famil-- ~~~
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complement(20832._.2)
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                                                                                                                     complement (21402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(18051. .18348)
/rpt_family="Aluy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="DDS similarity to N20479 yx39g09.sl Homo sapiens DNA clone 264160 3'. Score: 900 Identity: 455/460
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finger protein [Homo sapiens] (474. .726)."
15272. .15565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THQQSHTGESPFKLRECGKDFNKCNTGQRQKTHTGERSYECGESSKVFKYNSSLIKH
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. .22100
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. .18050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koop, B.F., Rowen, L., Wang, K., Kuo, C.L., Seto, D., Lenstrande, P. and Hood, L.
The human T-cell receptor TCRAC/TCRDC (C alpha/C delta)
organization, sequence, and evolution of 97.6 kb of DNA
Genomics 19 (3), 478-493 (1994)
                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 251124)
Boysen, C., Simon, M.I. and Hood, L.
Analysis of the 1.1-Mb human alpha/delta T-cell receptor locus with
bacterial artificial Chromosome clones
Genome Res. 7 (4), 330-338 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 251124)
                                                           Submitted (20-JUL-1997) Department of Molecular Biotechnology, University of Washington, Box 357730, Seattle, Washington 98195,
                                                                                                                                     This citation covers bases 1-983545 and bases 1064020-1071650 (bases 1 to 251124)
                                                                                                                                                                                                       T-Cell Receptor Alpha Delta Locus Complete
                                                                                                                                                                                                                                           3 (bases 1 to 251124)
Boysen, C., Inyoul, L., Smith, T.M., Smit, A., Wang, K., Rowen, L. and
    delta
                     Complete nucleotide sequence of the human T-cell receptor alpha
                                                                                                 Boysen,C., Lee,I., Smith,T.M., Smit,A., Kai,W., Direct Submission
                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                               This citation covers from bases 966383-1064019
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Pred. No. 9.1e-31;
0; Mismatches 42;
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                                                                                                                        Lee, R. and Leroy,
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        complement (5366. .5574)
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/note="Old_name_TCRAV12S1"
join(<11900. .11948,12152.
/gene="TCRAV19S1"
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/gene="TCRAV18S1"
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/note="heptamer"
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|gene="TCRAV19S1"
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/ETRDTTYYLFWYKQPPSGELVFLIRRNSFDEQNEISGRYSWNFQKSTSSFNFTITAS
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DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USJ 3 (bases 1 to 99108)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                 Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 28, 2001 this sequence version replaced gi:7709249. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 99108)

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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Homo sapiens chromosome 5 clone CTB-35A8,
AC008666
                Quality: Phrap Quality >=40 99.6% of Sequence; Estimated Total Number of Errors is 0.3.
                                              www-shgc.stanford.edu
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Finishing Completed at Stanford Human Genome Center
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Direct Submission
Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mi
Submitted, Walnut Creek, CA 94598, USA
On Aug 23, 2001 this sequence version replaced gi:10944452.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                   Direct Submission
Submitted (21-0CT-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 176629)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                         Submitted (03-AUG-1999) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 3 (Dases 1 to 176629)
DOE Joint Genome Institute and Stanford Human Genome Cer
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DOE Joint Genome Institute.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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SOURCE
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                                              -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                             Direct Submission
Submitted (12-AN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (Dases 1 to 205819)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                         AC106805.1 GI:18139355
HTG; HTGS_PHASE1; HTGS_DRAFT;
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                AC106805 205819 bp DNA linear HTG 25-JAN-200:
Homo sapiens chromosome 5 clone RP11-507E2, WORKING DRAFT SEQUENCE.
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WI-5180 G02907
SHGC-10972 G11217
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Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.8.
                                Web site: http://www.jgi.doe.gov
                                                                                                                                                     2 (bases 1 to 205819)
DOE Joint Genome Institute.
                                                                                                                                                                                      Sequencing of Human Chromosome Unpublished
                                                                                                                                                                                                                                                                                             Homo sapiens
Project Information
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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Pred. No. 2.4e-30;
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RESULT 11
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Estimated insert size: 210100; agarose-fp estimation
Quality coverage: 205419; sum-of-contigs estimation
Quality coverage: 9.07 in Q20 bases; agarose-fp estimation

**NOTE: This is a 'working draft' sequence. It currently

**consists of 5 contigs. The true order of the pieces

**is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              898
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HS1112F19 116368 bp DNA linear PRI 11-MAR-20 Human DNA sequence from clone RP5-1112F19 on chromosome 20q13.13-13.2 Contains the gene for a novel protein similar to SALL1 (sal (Drosophila)-like 1) (LOC57167), ESTs, STSs, GSSs and
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/clone_lib="RPCI human BAC library
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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13725: gap of unknown length
31289: contig of 17564 bp in length
31389: gap of unknown length
61952: contig of 30563 bp in length
62052: gap of unknown length
106299: contig of 44247 bp in length
106399: gap of unknown length
205819: contig of 99420 bp in length
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Pred. No. 4.8e-30;
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AUTHORS
TITLE
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RP5-1112F19 is from the library RPCI-5 constructed by the group
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORMPEP there.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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On Jul 23, 1999 this sequence version replaced gi.5566333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL034420.16 GI:5578919
HTG; CpG island; LOC57167; SALL1
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AL034420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is the entire insert of clone RP5-1112F19.
Location/Qualifiers
                                                                         note="TIGGER1 repeat: matches 1169. .1299 of consensus"
                                                                                                                                                                                       note="TIGGER1 repeat:
                                                                                                                                                                                                                                         note="MER41A repeat: matches 5. .554 of consensus"
                                                                                                                                                                                                                                                                                                    note="TIGGER1 repeat: matches 1431. .1692 of consensus"
                                                                                                                                                                                                                                                                                                                                                            note="AluJb repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                 note="TIGGER1 repeat: matches 1686. .1829 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluY repeat: matches 1.
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                                                                                                                                 note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="TIGGER1 repeat: matches 1973. .2156 of consensus"
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/clone_lib="RPCI-5"
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mol_type="genomic DNA"
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                                                                                                                                                                                       matches 1299.
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                                                                                                                                    . 294
                                                                                                                                                                                                                                                                                                                                                            .137 of consensus"
                    .292 of consensus
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4679. .4971
QKAĞSÖĞLİLDALKQAKLPANI PSATISLSPGLAPFTLKPDGTRVLPNVMSKLPSAL
LPQAPGSVLFQSPFSTVALDTSKKGKKERPINI SAVDVKRKDEAALYKHKCKYCSKVFG
TDSSLQIHLKSHTTGERE PYCSVCGHRETER TYKSUKVHFHRH PQVIÇANPQLFABFQDLVA
AGNGI PYALSVPDP I DEPSLSLDSKPVLVTTS VGLPQNLSSGTINPKDLTGGSLPGDLQ
PGPS PEBEGGPTLPGVCENYNIS PRAGGFQGSGTPE PGSTILKLQQLVERI DKATTDPN
BCLL CHRVLSCQSSLKMYKTHTIGERE PPQKIK CIÇRAPSTKGNLKTHLGVHFTNTS IKT
QHSCP I CQKKFTNAVMLQOHIRMHMGGQI PNTPLPENPCDFTGSEPMTVGENGSTGAI
CHDDVL IES I DVEEVSGBAPSSSSKVPTPLPS HASDE PTGTANGASLDAPGKVGPAP
FNLQRQGSRERENGSVESDGLTNDSSSKVPTPLPS HASDE PTGTFTGALSPANSQAESI
KSKSPDAGSKAESSENSRTENEGRSSLPSTFIRAPPTYVKVEVPGTFVGPSTLSPGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 match: EST8: Em:AI632569 Em:AI638036 Em:AA417660"
/evidence=not_experimental
complement(6825)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3048. .3268

/note="AluSp repeat: matches 1. .221 of consensus"

3135. .3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: proteins: Tr:Q91929 Tr:Q99881 Tr:Q62255 Tr:Q43340 Tr:O12958 Sw:P51508 Tr:Q96395 Tr:Q9Z117 Sw:P39770 Sw:P39806 Tr:P91639 Tr:Q24219 Tr:Q95878 Sw:P18746 Tr:Q90658"
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[note="12 copies 2 mer aa 100% conserved"]
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/note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APVNHPGNIÐVASÐÐBATVKRLRRESTHVCEKCCABEFESÍSEELEHKKNGTKNEPVLI
MNDSBGPVPSBDFSGAVLSHQPTSPGSKDCHRENGGSSBDMKBKPDABSVVYLKTETA
LPPTPQDISYLAKGKVANTNVTLQALRGTKVAVNQRSADALFAFVPGANSIPWVLEQI
LCLQQQQLQQIQTEQIRIQVNMMASHALHSSGAGADTLKTLGSHMSQQVSAAVALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
protein similar to SALL1 (sal
(prosophila)-like 1) (LOC57167))"
/protein_id="CAB61485.1"
/db_xref="G1:6456821"
/db_xref="G01:6456821"
/db_xref="G01:6456821"
/db_xref="G01:040"
/db_xref="G01:05wiss-Prot:Q9UJQ4"
/db_xref="WSRRKQAKPQHINSEEDQGEQQPPQQTPEFADAAPAAPAAGELG
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/gene="dJ1112F19.1"
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2714. .3017
/note="AluSp repeat: matches 1. .304 of congensus"
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note="Single clone region. Single cloned region in
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/note="TIGGER1 repeat:
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note="AluSg repeat: matches 2.
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                   973
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                                                                                                                                                                                                                                                                                                                    251;
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                            TCCAGGGGCTGGGCGGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGCCGAGGCA 798
                                                    CÁGGAGGCTGACTCAGGAGAATCACTTAAACCTGGGAGATGGAGGTTGCAGTGAGCCGAG 7005
                                                                                                                                                                                                                    GGTGGATCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAAACGTTGTC
                                                                                 CAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTGA-----
                                                                                                                    TCTACTAAAAAACACAAAAATTAGCCGGGGGTGGTGGTGACACATCTGTAATCCCAGCTACT
                                                                                                                                                                                   GGAGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCTGTC
                                                                                                                                                                                                                                                     TCAAAGGGCTGGGCGTGGTGGCTCGTGCCTGTAATCCCAGCACTTTGGGACGCTGAGGTG
                                                                                                                                                  TCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCTACT
                                                                                                                                                                                                                                                                                                                        Conservative
/note="match: GSS: Em:AQ341439"
complement(14576. .15010)
/gene="dJ1112F19.1"
                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSp repeat: 17440. .17615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJo repeat:
complement(14508. .15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSq
9924. .10198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9335. .9586
/note="L1MD2 repeat: matches 6084. .6341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8873. .9176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluJb repeat: matches 1.
16284. .16511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATDGVPKHQFPHFLEENKIAVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSMLNGGLAVKTNEISVIQSGGVPTLPVSLGATSVVNNATVSKMDGSQSGISADVEKF
                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 45. .244 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: 15825. .16275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="dJ1112F19.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="FLAM_C repeat: matches 1. .0623. .10905 repeat: matches 3. .note="AluJo repeat: matches 3. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177. .9314
note="AluJo repeat: matches l. .136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="AluSc repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7578. .7803
/note="MER47A repeat: matches 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .256 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSx repeat: matches 1. .274 of consensus" 0466. .10589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluJo repeat: matches 136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER47A repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluSx repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5190. .15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1506. .11546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluY repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJo repeat: matches 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match: STS: Em:N72278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match: GSS: Em:AQ341889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0948. .11191
                                                                                                                                                                                                                                                                                                                                      82.0%;
                                                                                                                                                                                                                                                                                                                                                     19.6%;
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Pred. No. 5.5e-30;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 1. .309 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                         matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 1.
                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .296 of consensus"
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REFERENCE
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Gollins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Merwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Muzphy, T., Naylor, J., Nguyen, C., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Ve, W.J., Young, G., Viell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalinoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone CTD-2193U24
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                 320 Charles Street,
                                                                                                 (17-AUG-2002) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                          Zimmer, A. and Zody, M.
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Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardya, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C.H., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuer, J., Peterson, K., Teffaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, N., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

N. Submitted (13-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 13, 2002 this sequence version replaced gi:22296745.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Center project name: L25381

Center colone name: 2193_J_24
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Only the first 159.5 kilobases of this clone are being submitted. The remainder overlaps accession number AC003042 [WICGR project 1260].

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complement(10880. .10989)
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/rpt_family="AluSx"
15961. .16045
                                                                                   complement (11056.
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complement(5095. .5617)
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                                                                    adı/
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                                                                                                                                                                                                                                                                                                                         _family="AluSg/x"
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                                                     eggecTeggcGCGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGCCGAGGCAGGTG
                          GGGGCCAGGCGTGGTGCACACCTGTAATCCTAGCACTTTGGGAGGCCGAGGTGGGAG
                                                                                  Conservative
                                                                                                                                     complement (30024...30125)
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complement (30126...30263)
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complement (30264...30551)
                                                                                                                                                                                                        complement (29419. .29571)
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complement (29583. .29744)
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complement (29794. .29997)
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complement (20468. .21174)
/rpt_family="HUERS-P2"
complement (21174. .24069)
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                                                                                                                                                                                                                                                                                                                                                                                                                complement (28259.

/rpt family="AluJo

complement (28442.

/rpt family="LIME1

28556. 28648.
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compTement(28644. .. 28949)
/rpt_family="AluSx"
28950. . 28994
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complement(24365,
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/rpt_family="MIR"
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complement(19244. .20030)
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complement(19056. 19189)
/rpt family="LTR28"
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complement(16770.
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7. .28542
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ement (20...
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ement(2017)
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ement(28447
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Homo sapiens BAC clone RP11-41E15 from
AC108026
AC108026.5 GI:1938770'
                                                                                                     Submitted (13-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Mar 13, 2002 this sequence version replaced gi:18873888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133902)
Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 123902) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desai, A. and Cotton, M.
The sequence of Homo sapiens
Unpublished (2001)
                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                      MO 63108, USA
5 (bases 1 to 123902)
                                                                                                                                                                                                                                                                                                              MO 63108, USA
4 (bases 1 to 123902)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 123902)
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0041E15
                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC
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Missouri 63108,
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality 30); an attempt was made to resolve all sequencing problems, suc

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

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FEATURES
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Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-811L19; the clone sequenced to the right is RP11-270L13, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-41E15; actual end is at base position 52485 of RP11-270L13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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3444. .3012
                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich"
6918. .7076
                                                                                                                                                                                                                                                                       /rpt_family="MER2_type"
7377. .7401
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/clone_lib="RPCI-11"
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L0706. .11007
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                                                                                                                                                                                                                                                                                                                                                                             rpt_family="L2"
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_xref="taxon:9606"
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family="L1"
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                                                                            On Feb 28, 2002 this sequence version replaced gi:1855988.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP http://www.sanger.ac.uk/Pprojects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/SPC/Chr10

RP11-164C1 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.sanger.ac.uk/SPC/Chr00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA
IMPORTANT: This sequence is not the entire insert of clone RP11-164C1 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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Pred. No. 7.8e-30;
0; Mismatches 47;
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The true left end of clone RP11-164C1 is at 1 in this sequence. true left end of clone RP11-363N22 is at 131861 in this sequence. The true right end of clone RP11-809C18 is at 76104 in this
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                                                                                                                                                                                                                                                                       19.5%;
Similarity 82.3%;
                                                                                                                                                                                          CAGGGGCTGGGCGCGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGCCGAGGCAGG
                                                                                                                                                    CATGGGAGGGGCACGGTGATGCCTGTAATCCCCCACGCTTTGGGAGGCCGAGGCGGG 89434
TACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCTACTCA 920
                                                     TGGATCACCTGAGGTCGGGAGTTTGAGACCAGCCTGACCAACATGGTGAAACTCTGTCTC
                                                                                 TGGATCACTTAAGGTCAGGAGTTTGAGACCCAGCCTGCCCAACATGGTGAAACGTTGTCTC 860
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                        64558. .64688
/note="Sequence from overlapping clone RP11-809C18
(AL358216). Assembly confirmed by restriction digest."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Reads generated from a transposon library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="RPCI-11.1" 2368. - 2990
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Single clone region. Assembly confirmed restriction digest data."
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AL358216). Assembly confirmed by
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/chromosome="10"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                Score 202.4; DB 9
Pred. No. 9.3e-30;
0; Mismatches 46
                                                                                                                                                                                                                                                                                                DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone RP11-809C18
/ restriction dige
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JOURNAL 65335 bp Homo sapiens BAC clone RP11-692E14 AC112698 AC112698.4 GI:21326424 HTG. Harris, A. and Meyer, R. The sequence of Homo souppublished (2001) 1 (bases 1 to 65335)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Homo sapiens 99063792 Homo sapiens (human) (bases 1 to 65335) sapiens BAC clone Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. from 4 complete linear sequence. PRI 26-JUN-2002

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Submitted (26-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6:
On Jun 5, 2002 this sequence version replaced gi:20340530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-APR-2002) Genome University School of Medicine, MO 63108, USA 5 (bases 1 to 65335) Waterston, R.H.
                                                            There is a single plasmid region from 24260 to 24349. Polymorphisms have been identified between AC107214 and AC112698. Data from AC114911 was used to finish this clone, AC112698.
                                                                                                                                                            NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-451F20, 2000 bp overlap;
the clone sequenced to the right is RP11-367N14. Actual start of
                                                                                                                                                                                                                                            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong vectors: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Submitted (05-JUN-2002) Genome
University School of Medicine,
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Direct Submission
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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                                                                                                                                           clone is at base position 114362 of RP11-451F20.
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New isolated human genes and the secreted polypeptides they encode -

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CC or ameliorating medical conditions, e.g. by protein or gene therapy.

CC Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each polymucleotide, based on which tissues they are most highly compressed in, and include developing products for the diagnosis or creatment of cancer, immune disorders, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autoimmune conditionations, allergy, hematopoietic disorders, sethma, immunodeficiency cord injuries, allergy, hematopoietic disorders, skeletal disorders, arthritic disorders, skeletal disorders, arthritic disorders, asthma, immunodeficiency cord injuries, and transplant rejection. The polypeptides are also useful for identifying their binding partners

Sequence 1038 no. ~~~
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GCTTTTGCTAAATTGTTACCTGACAAAATCTTAGCCAGTTCTTCATTTTCGTTTTGAGAT
                                                                                                         ATATAAGGATGTGAGGAGGACTACAAAACAGGAAAAAATAAACAGATTTCGTTTGTG
                                                                                                                                                                                                                GATGAGATCTACAGTGTAGGCAAACTTATATAATCTGTCAACTCCATTAGTGTCATAGTC
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Claim 1; Page

726; 785pp; English.

The invention relates to novel genes (ABQ92553-ABQ92607) and proteins (ABP62013-ABP62153) useful for preventing, treating or ameliorating

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                                                                                                                                                       New polynucleotides and polypeptides useful for diagnosing, prognosing treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or dispress.
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Matches 1038
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CC The present invention relates to novel human secreted proteins (ABR47633-CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins CC and their coding sequences are useful for the preparation of a diagnostic CC or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tabhycardia, cardiac arrest, coronary CC arteriosclerosis and myocardial ischaemia), neural disorders, immune CC system disorders, muscular disorders, reproductive disorders, for CC gastrointestinal disorders, pulmonary disorders, renal disorders, for CC considerative disorders and/or cancerous diseases and conditions, for confection, for treating thrombosis and arteriosclerosis, for treating or CC infection, for treating thrombosis and arteriosclerosis, for treating or CC constituted damage which occurs in neuronal disorders or CC neurodegenerative conditions such as Alzhaimer's disease and Parkinson's CC disease, to enhance bone and periodontal regeneration and aid in tissue ctransplants or bone grafts, to prevent skin aging or hair loss, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             문
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                                                                                                                                                                                                                                                                                                          Novel human secreted proteins, useful diagnosing, prognosticating, treating disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-0277340P
19-JUL-2001; 2001US-0306171P
13-NOV-2001; 2001US-0331287P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; antiinflammatory; nootropic; neuroprotective;
antiparkinsonian; gene therapy; human; cardiovascular disorder;
                                                                                                                                                                                                                                                                             Claim 21; SEQ ID NO 36; 1881pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2002; 2002WO-US009785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
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and/or ameliorating cardiovascular
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XX 밁 Ş 밁 Ş 밁 S WO200276488-A1 Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; antiinflammatory; Human secreted protein-encoding gene 15 cDNA clone HBIAE26, SEQ ID NO:25 ABZ71204 1021 961 961 901 901 841 standard; AAAAAAAAAAAAACTCGA 1038 AGGTTGCAGTGAGCCATTGCACTCCAGCCTGGGCAACACAGTGAGACTCTTGTCTCAAAA TCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAG TCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAG ACATGGTGAAACGTTGTCTCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACA immunosuppressive; vulnerary; gene therapy; gene; ss. CDNA; 1020 1020 960 900

21-MAR-2001; 2001US-0277340P. 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P. 03-OCT-2002 19-MAR-2002; 2002WO-US008276. (HUMA-) HUMAN GENOME

New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.

2003-029900/02.

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Claim 21; Page 764-765; 1216pp; English

CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted CC protein genes, and ABP0011-ABP00299 represent the proteins they encode. CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The CC invention also encompasses antibodies specific for the secreted proteins, cities and host cells comprising a nucleic acid of the invention. The Secreted proteins, nucleic acids encoding them, antibodies or antibody CC fragments specific for the secreted proteins, and mediorating or preventing CC digestive disorders. Such conditions include disorders of protein CC digestive disorders. Such conditions include disorders of the mouth, CC oscophagus, stomach, small intestine, large intestine, liver, biliary CC tract and pancreas, and include cancers of these organs and tissues. The Secreted proteins and their nucleic acids may also be used in the CC treatment of immune disorders, inflammation, infection, Nucleic acids of the invention may be used for chromosome identification, chromosome

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TCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAG
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                                       ACATGGTGAAACGTTGTCTCTACTAAAAATACAAAAATTAGACAGGCGTGCTGGCACACA
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                                                                                                                                                                                                                                                          The invention relates to isolated nucleic acid molecules ADB91055-CC ADB91848 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-CC ADB91834. Also disclosed is a recombinant vector comprising a CC polynucleotide of the invention, and a recombinant host cell comprising CC the recombinant vector. The polypeptide of the invention is useful in CC identifying a binding partner by contacting the polypeptide with a binding partner, and determining whether the binding partner increases or CC decreases activity of the polypeptide. The polypeptide, polynucleotide, CC antibody or its fragment, agonist or antagonist are useful for preparing CC a pharmaceutical composition for diagnosing or treating diabetes or CC conditions related to diabetes. The present sequence is that of the human CC the stability of the fused protein as compared to the secreted protein CC conly. Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                    Query Match
Best Local Sim
Matches 1038;
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                                                                                                                                                                                                            Sequence 1038 BP; 328 A; 167 C; 198 G; 339 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9;
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19-JUL-2001; 2001US-0306171P
13-NOV-2001; 2001US-0331287P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-2002; 2002WO-US008124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cances atherosclerosis).
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                               Sequence
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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-cassociated proteins. Also included are an expression vector comprising the isolated nucleic acid or expression vector, a microarray for detecting creambinant nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above-comprising at least one probe comprising the above polypeptide, a hybridoma that produces the above antibody and a pharmaceutical composition comprising the above comprising the antibody, a pharmaceutical composition comprising the above concordidated antibody, a pharmaceutical composition comprising the above of ror detecting the presence or absence of cancer cells in an comprising the presence or absence of cancer cells in an comprising the presence or absence of cancer cells in an comprising the protein (CAP), methods for detecting cancer cells in an individual, a method for inhibiting growth of cancer cells in an comprising cancer activity or for a bioactive agent capable of modulating the activity of a CA protein (CAP), methods for detecting cancer cells in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and cell-without of the printed sequence. Note: The sequence data for this patent did not form part of the printed cell ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2003; 2003US-00367094.

14-MAR-2003; 2003US-0038838.

15-APR-2003; 2003US-00417375.

13-JUN-2003; 2003US-00461862.

15-SEP-2003; 2003US-00663431.

15-DEC-2003; 2003US-00737318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 16; seqid 434; 310pp; English.
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Sequence 68196 BP; 20295 A; 14326 C; 13150 G; 20385 T; 0 U; 6

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ABD32800 standard; DNA; 68196

18-NOV-2004 ABD32800;

(first entry)

Query Match Best Local Similarity Matches 245; Conserv Conservative 19.3%; 0; Mismatches Score 200; Pred. No. 4. 50; Length Indels 5 Gaps

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                                                                                                       partient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT11112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the mallgnant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent did not form nart of the vicintal special sequence and the patent did not form nart of the vicintal special sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing breast cancer in a patient comprises detecting the legene expression in cell or tissue samples, where a differential expression is indicative of breast cancer.
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25-APR-2001; 2001US-0286090P
23-MAY-2001; 2001US-0292517P
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                               ftp.wipo.int/pub
                                                              did not form part of the printed specification, electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods of diagnosing breast
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22-OCT-2001;
07-JAN-2002;
08-FEB-2002;
08-FEB-2002;
                                                                                                                                                                                     Human; ALMS1; chromosome 2; 2p13; Alstrom disease; retinal dystrophy; cardiomyopathy; endocrinopathy; diabetes; Alstrom syndrome; cardiant; ophthalmological; antidiabetic; hepatotropic; nephrotropic; gene ther
          (UYSO-) UNIV
                                                                                           15-OCT-2002; 2002WO-GB004658
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Pred. No. 7.8
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210000
310000
354391
BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method of diagnosing the presence of, CC or susceptibility to, retinal dystrophy, cardiomyopathy, endocrinopathy, CC diabetes, or Alstrom syndrome in an individual. The method comprises CC typing in a sample from the individual the ALMS1 protein or ALMS1 gene CC ALMS1 is located to chromosome 2, more specifically to 2pi3. ALMS1 has CC ophthalmological, cardiant, antidiabetic, hepatotropic and nephrotropic CC activities, and can be used in gene therapy. The method is useful for CC diagnosing the presence of, or susceptibility to, retinal dystrophy, CC cardiomyopathy, endocrinopathy (e.g. liver disease or renal impairment), CC diabetes, or Alstrom syndrome in an individual. ALMS1 sequences can be CC used in an agent that prevents or treats retinal dystrophy, CC cardiomyopathy, endocrinopathy or diabetes is useful in manufacturing a CC used in an agent that prevents or treats retinal dystrophy, cardiomyopathy, endocrinopathy or diabetes is useful in manufacturing or Desing susceptible to retinal dystrophy, cardiomyopathy, endocrinopathy or diabetes. ACF42332 to ACF42747 and ABR82113 to ABR82118 represent for the avenual fiftering of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                         Matches 234;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences used in the exemplification of the present invention
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                        GGGGCTGGGCCCGATAGCTGATGCCTGTGGTCCCAGTGCTTTGCGGGGCCCGAGGCAGGTG
                                                                                                                                                                                                                                                         GATCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAACGTTGTCTCTA
CTAAAAATACAAAAATTAGCCGGGTGTGGTGGCACGCGCCTGTAATCCCAGCTACTTGGG
                                                                                                                                                                                                                               GATAACCTGAAGTCAGGAGTTCAAGACCAGCCTGGCCTACATGGTGAAACCCCTGTCTCCA
                                                                             AGGCTGAGGCAGGAGATCTCTTGAATCTGGGAGGCGGAGGTGGCAGTGAGCCACTGCAC
                                                                                                                 AGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCATTGCAC
                                                                                                                                                                                        CTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCTACTCAGG
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   19.2%;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 199.2; DB:
Pred. No. 8.1e-33,
0; Mismatches 58
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RESULT 11
ABD32548/c
ID ABD32548;
XX ABD32548;
XC ABD32548;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated genomic DNA HD14-033.
XX
DE Human; ds; cancer-associated protein; gene; cytostatic;
XX
COS Homo sapiens.
XX
PN W02004074320-A2.
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cancer;

02-SEP-2004.

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CC an open reading frame of a CA sequence selected from any of the 95 cc polynucleotide sequences as mentioned in the specification, or its C complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above CC entibody and a pharmaceutical composition comprising the above CC entibody and a pharmaceutical excipient, a kit for detecting cancer cc colls (comprising the antibody cited above, methods for diagnosing cancer cc individual, a method for inhibiting growth of cancer cells in an CC individual, a method for inhibiting growth of cancer cells in an CC individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above CC polynucleotide or polypeptide (or their fragments), methods of screening CC for anticancer activity or for a bioactive agent capable of modulating cancer in a cell. The composition and methods for detecting cancer cells associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of CA gene in a cell. The composition and methods are useful for detecting, Cd diagnosing, preventing and treating cancers, especially lymphoma and cell cancer. The present sequence is a human CAP genomic sequence. Note: The sequence data for this patent did not form part of the printed concers. The present sequence is a human CAP genomic sequence. Note: The sequence data for this patent did not form part of the printed concers. The present sequence is a human CAP genomic sequence. Note: The sequence data for this patent did not form part of the printed concers.
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14-MAR-2003; 2003US-0038838.
15-APR-2003; 2003US-00441375.
13-JUN-2003; 2003US-00461862.
15-SEP-2003; 2003US-00663431.
15-DEC-2003; 2003US-00737318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 23 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above recombinant nucleic acid cited above, a host cell comprising the above recombinant nucleic acid cor expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above-mentioned nucleotide sequences, an isolated polypoptide (encoded within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 310268 BP; 87522 A; 60932 C; 62901 G; 98913 T; 0 U; 0 Other;
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ANAATACAAAATTAGCCAGGCATGGTGGTTGGCACCTGTAATCCCAGCGACTCGGGAG 140298
                             AAAAATACAAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCTACTCAGGAG 924
                                                                                                                       TCACTTRAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAACGTTGTCTCTACT
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14-AUG-2000
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; gene therapy;
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17-MAR-2000;
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2000US-0227009P.
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2000US-0229343P.
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2000US-0226279P.
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RESULT 13
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AC ABL97
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01-DEC-2000
01-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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11-DEC-2000;
05-JAN-2001;
  21-JUN-2002
                         ABL97825;
                                               ABL97825 standard; DNA; 32249
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
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ilarity 81.9%;
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2000US-0249245P.
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2000US-0249297P.
2000US-02492997P.
2000US-0249300P.
2000US-0250391P.
2000US-0251030P.
2000US-02517988P.
2000US-0251798P.
2000US-0251866P.
2000US-0251869P.
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2000US-0251989P.
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 (first entry)
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                                                                                                                                                                                                                                                                                                                                                   Score 198.2; DB Pred. No. 1e-32; O; Mismatches
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2000US-024652P.
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X
Human testicular antigen (reproductive system disore (cardiovascular disorder; gastrointestinal disease; Homo sapiens. WC200155317-A2. 02-AUG-2001. 117-JAN-2000; 2000US-01806; 24-FEB-2000; 2000US-01863; 16-MAR-2000; 2000US-01863; 16-MAR-2000; 2000US-01863; 17-MAR-2000; 2000US-01863; 17-MAR-2000; 2000US-01863; 17-MAR-2000; 2000US-01863; 17-MAR-2000; 2000US-01981; 11-JUL-2000; 2000US-02166; 11-JUL-2000; 2000US-02166; 11-JUL-2000; 2000US-02168; 11-JUL-2000; 2000US-02
testicular antigen encoding DNA fragment SEQ ID NO: 2477. testicular intigen; testes, cancer; metastasis; immune disorder; wascular disorder; respitantory disorder; metastasis; immune disorder; particular disorder; respitantory disorder; neurological disorder; intrestinal disease; infection; cytostatic; gene; da. disorder; intrestinal disorder

14-SEP-2000 11-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 25-SEP-2000 25-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 21-CCT-2000 21-CCT-2000 20-CCT-2000 21-CCT-2000 20-CCT-2000 20-CCT
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Matches 245
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                   Transcript; therapy; systemic lupus erythematosus; inflammatory disease; cardiovascular; gastrointestinal disease; atherosclerosis; skin disease; rheumatoid disorder; autoimmune disease; diabetes; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary syste reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a
 05-JUN-2003
                                                                         cancer; neuroprotective; human; 76P; antisense; gene; ds.
                                                                                                                                                             22-SEP-2003
                                                                                                                                                                                    AAL61140
                                                                                                                                                                                                             AAL61140 standard;
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                         WO2003046220-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids encoding 973 human testicular antigen polypeptides, venting, diagnosing and/or treating testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment of the invention
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Pred. No. 1e-
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RESULT 15 ADM98105 ID ADM98

ADM98105

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to methods and systems for identifying naturally occurring antisense transcripts. The method is useful for quantifying gene expression levels and for detecting, quantifying or specifically regulating antisense and respective sense transcripts thereby enabling detection and treatment of a wide range or disorders, such as systemic lupus erythematosus, inflammatory diseases, rheumatoid disorders, autoimmune diseases, diabetes, multiple sclerosis, cardiovascular and gastrointestinal diseases, atherosclerosis, skin diseases and cancer. T present sequence is human 76p antisense transcript DNA used to illustra the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying putative naturally occurring antisense transcripts, useful for quantifying gene expression levels, and detecting and/or treating inflammatory, autoimmune or cardiovascular diseases, diabetes, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-2001; 2001US-00993398
24-JUL-2002; 2002US-00201605
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                                                                                                                                        GCGTGGTGGCACACATCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAATTCCTT
                                                                                                                                                                                                   AGACCAGCCTGCCCAACATGGTGAAACGTTGTCTCTACTAAAAATACAAAAATTAGACAG
                                                                                                                                                                                                                                                      CCTGTGGTCCCAGTGCTTTGCGGGGCCGAGGCAGGTGGATCACTTAAGGTCAGGAGTTTG
                                                                                                                                                                                                                                                                                          AATTCTAGCTAATGAAAATATACTTAAAAGTATTTCTTAGGCCGGGCATGGTGGCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTTTTTTATTAATATATAAGGATGTGATGAGTATGACTACAAAACAGGAAAAAATAAA
                            ААСАСАСТСАСАСТСТТСТСТСАЛАЛАЛАЛАЛАЛАЛА 1033
                                                         GAACCTGGGAAGCAGACGCTGCAGTGAGCTGAGATTGTGCCATTGCATTCCAGCCTGGGC
                                                                                      GAACCTGGGAGGCAGAGGTTGCAGTGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                            AAAGTAATTATGTTTATAAATAGACTAACTGCTGGATGTTACCACCAAGTAAGAAAGCAA
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Bernstein J,
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Dahari
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Pred. No. 1.5e-32;
D; Mismatches 144;
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Wasserman
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                                                                                    GCCATTGCACTCCAGCCTGGGC
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The invention relates to identifying putative naturally occurring CC antisense transcripts (NAS) by computativally aligning a first database of of sense-oriented polynucleotide sequences with a second database of CC expressed polynucleotide sequences, identifying expressed polynucleotides (CC forming a duplex with sense-oriented polynucleotides, or screening a CC database of expressed polynucleotide sequences based on a sequence CC criterion selected to identify NAS. Also included a kit for quantifying an NAS of CC interest, designing artificial antisense transcripts using a database of NAS, a computer readable storage medium comprising a database of System for generating a database of several of NAS, quantifying an mRNA of interest in a biological sample, quantifying the expression potential CC interest in a biological sample, quantifying an abnormal CC interest in a biological sample, quantifying an abnormal phenotype and comparing the expression level of NAS of interest in cells having an abnormal phenotype with an expression level cells having a community and another comparing the expression level of NAS of interest in cells having an abnormal phenotype, treating or preventing a first condition or syndrome associated with an up regulation of NAS complementary to a naturally occurring mRNA transcript and diagnosing a disease, condition or syndrome associated with a standard expression ratio of an mRNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying putative natural antisense transcripts by aligning database having sense-oriented polynucleotide sequence with database of expressed polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 88; natural antisense sequence; diabetes; autoimmune disease; Parkinson's disease; Alzheimer's disease; HIV infection; malaria; cholera; influenza; rabies; diphtheria; breast cancer; colon cancer; cervical cancer; melanoma; lung cancer; ovarian cancer; pancreatic cancer; prostate cancer; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEVA/)
(POLL/)
(NEMZ/)
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11-DEC-2000;
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(KHOS/)
(WALA/)
(LEVI/)
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18-JUL-2001;
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Dahari D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4165 BP; 1123 A; 994 C; 954 G; 1094 T; 0 U; 0 Other;
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ALIGNMENTS

RESULT 1

US-09-949-016-12026

Application US/09949016

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FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FRANKSEQ for Windows Version 4.0

SEQ ID NO 12026
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local S
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 168104
TYPE: DNA
ORGANISM: Human
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NAME/KEY: misc feature
LOCATION: (1)...(168104)
OTHER INFORMATION: n = A,T,C
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256 CAAAACCTTGTTAGTTTTTAGGGTATAGTCACATTTTATAAATGTGCGGTATATTTATAC 315
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                                                                AGCATGAAAATAACATATCTAATATTTTGTGACTATCTTATTAGGAAAAATCAGAGAATTT 255
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Pred. No. 8.5e-237;
5; Mismatches 4; Indels 0; G
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Sequence 16554, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/247,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 16554

LENGTH: 168105
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US-09-949-016-16554
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; CGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(168105)
; OTHER IMPORMATION: n = A,T
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                                                                       GTCTCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCCAGCT
                                                                                                                                   GCAGGTGGATCACTTAAGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGTGAAAACGTT
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       ACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCC
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99.1%;
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Pred. No. 8.5e-237;
5; Mismatches 4;
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j LENGTH: 601
j TYPE: DNA
j ORGANISM: Human
US-09-949-016-170431
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
PILE REFERENCE: CL001307
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-09-08
PRIOR FILING DATE: 2000-09-09-08
PRIOR FILING DATE: 2000-09-09-08
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PRIOR FILING DATE: 2000-09-09-09-09-
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US-09-949-016-170431/c
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Best Local Similarity
Matches 595; Conserv
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APPLICANT: VENTER, J.
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                              GGTCATTATCACCAAGTCTTCAAGGKATTACATTATAAAAACCTTGGKTTTTATTCTTGT
                                                                                                                                                                                                                                           GACTCATCCCCATGCTAAAATTATAGTTGTKAAAAATACGCTTTTGTAAATAGTTGTGTTA
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GAATAACCGTTTTTT
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Pred. No. 7.8e-137;
6; Mismatches 0;
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RESULT 5 US-09-949-016-16503

Sequence 16503, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016

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Sequence 1848, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOSTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 12848

LENGTH: 51620
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(51620)
; OTHER INFORMATION: n = A
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Best Local Similarity
Matches 245; Conserv
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                    CGTTGTCTCTACTAAAAATACAAAAATTAGACAGGCGTGGTGGCACACATCTGTAATTCC
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                                                                   AGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCGGAG-----ATTG 9163
                                                                                                   AGCTACTCAGGAGGCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTG 971
                                                                                                                                        CCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGCATGGTGGTGCTGCACCTGTAATCCC
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Pred. No. 7.4e-39;
0; Mismatches 50;
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15231
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US-09-949-016-15231/c
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PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTMARE: FastSEQ for Windows Version 4.
SEQ ID NO 16503
LENGTH: 51621
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; NAME/KEY: misc_feature
; LOCATION: (1)...(51621)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-16503
                Query Match
Best Local Similarity
Matches 245; Conservat
                                                                                                               SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15231
LENGTH: 75799
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                                                                                                                                                                                                                                                                                                                                                       Sequence 15231, Application Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 245; Conserv
                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                        NUMBER OF SEQ ID NOS: 207012
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                   Conservative
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ilarity 81.7%;
Conservative
                             19.3%;
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                Score 200; DB 4;
Pred. No. 8.4e-39;
0; Mismatches 50
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Pred. No. 7.4e-39;
0; Mismatches 50;
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OF DETECTION AND USES
                                          Length 75799;
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Best Local :
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15449

LENGTH: 14345

TYPE: DNA

CRCANTEN Human
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US-09-949-016-15449/c
; Sequence 15449, Application US/09949016
; Patent No. 6812339
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Local Similarity 76.9%;
                                                                                                 AACCTGGGAGGCAGAGGTTGCAGTGAG-------CCATTGCACTCCAGCCTGGGCA
                                                                                                                                                                                                           CGTGGTGGCACACATCTGTAATTCCAGCTACTCAGGAGGCTAACACAGGAAAATTTCCTTG
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АСАСАGTGAGACTCTTGTCTCAAAAAAAAAAAAAAAAA 1033
                                                         AACCCAGGAGGCGGAGGTTGCAATGAGCCAAGATTGCACCATTGCACTCCAGCCTGGGTG 9695
                                                                                                                                                                          CATGGTGGCATGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTG
                                                                                                                                                                                                                                                                                          GACCAGCCTGGGCAACATGGTAAAACCTTGTCTACTAAAAATACAAAATTAGCCAGG
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Pred. No. 9.2e-39;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14345;
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RESULT 9
US-09-949-016-15443
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US-09-949-016-12316
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Sequence 15443, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.2
Best Local Similarity 76.9
Matches 260; Conservative
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SEQ ID NO 12316
LENCTH: 39243
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-33
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131748

; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-131748

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; SOFTWARE: FASTSEQ for Windows Version
; SEQ ID NO 15443
; LENGTH: 39243
; TYPE: DNA
; ORGANICM: Human
US-09-949-016-15443
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CHERENEN AND TEATURE CL
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                             CTGTGGTCCCAGTGCTTTGCGGGGGCCGAGGCAGGTGGATCACTTAAGGTCAGGAGTTTGA
                                                                      TTAAGTTTTCTTGTTAAGCATTTTAGAATTTGAGAATAGGCTGGGYGCGGTGGCTCACGC
                                                                                                            TTTCGTTTTGAGATGAAGATACTTAGTTTTAGTCCAGGGGCTGGGCGCGATAGCTGATGC 766
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 CTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGTGGATCACTTGAGGTCAGAAGTTTGA
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                                                                                                                                                   Conservative
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                                                                                                                                             Score 198.4; DB 4
Pred. No. 3.8e-39;
1; Mismatches 67
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Pred. No. 1.3e-38;
                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                   Length 601;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA

TYPE: DNA

TYPE: DNA
US-09-949-016-14222, Sequence 14222, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                    RESULT 12
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US-09-949-016-12758
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Best Local Similarity 81.9%;
Matches 245; Conservative
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ORGANISM: Human
-09-949-016-12758
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                                                                                                                                        GCTAACACAGGAAAATTCCTTGAACCTGGGAGGCAGAGGTTGCAGTGA-------G
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Pred. No. 2.4e-38;
0; Mismatches 43;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 45906
LENGTH: 601
TYPE: DNA
CORGANISM: Human
US-09-949-016-45906
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VMMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14222
LENGTH: 88736
TYPE: DNA
ORGANISM: Human
US-09-949-016-14222
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  Query Match 19.0
Best Local Similarity 79.0
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45906, Appl. Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ETILE REFERENCE: CL001307
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14
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                    19.0%;
Score 196.8; DB 4;
Pred. No. 9.4e-39;
0; Mismatches 52;
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Pred. No. 2.4e-38;
                                     DB 4;
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                                     Length 601;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13052
LENGTH: 20441
TYPE: DNA
ORGANISM: Human
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(20441)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13052
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US-09-949-016-13052
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Best Local Similarity 79.8%;
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TITLE OP INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OP INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE; CL001307
                                                               11804 CCTGTCGCTACTAAAATACAAAACTTAGCCAAGTATGGTGGCATGTACCTGTAATCCCA
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Pred. No. 3.2e-38;
0; Mismatches 52; Indels 11;
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; ORGANISM: Human
US-09-949-016-45905
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 45905
LENGTH: 601
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity
Matches 248; Conserv
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Pred. No. 1.2e-38;
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	AAU32155 AAW67997 AAG09358 AAB43188 AAB43188 ADB65455 ADI16586 ADN42240 ADI16588 ADN42242 AAG09360 ABG4827 ADN18428 AAW30160 ABG24605 ABG24605 ABG21806	472	358	193	391	234	733	322	432	1970	57	416	416	415	415	406	360	308	107	20	99
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	Aau32155 Aaw67997 Aag99358 Aab43188 Aab4541591 Adi16911 Adi16586 Adi16586 Adi16586 Adi16586 Adi116586 Adi116586 Adi116586 Adi116586 Adi116586 Adi19240 Aag99360 Abb64827 Adn18428 Aag921806 Abg21806 Abg21806 Abg21806 Abg21806 Abg918064844 Abg65847 Abb66583	ABB66583	ABP65847	AAG71944	ADB64644	ABG21806	ABG24605	AAY30160	ADN18428	ABB64827	AAG09360	ADN42242	ADI16588	ADN42240	ADI16586	ADI16911	ADB65455	AAB43188	AAG09358	AAW67997	AAU32155

ALIGNMENTS

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RESULT 1
AAY87141
ID AAY8
AXX AAX8
AC AAX8
AXX JAX8
AXX JAX8
AXX JAX8
AXX JAX8
AXX JAX8
AXX Huma
XXX Huma
XXX Huma
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WO200004140-A1. Homo sapiens.

14-JUL-1999; 27-JAN-2000. 99WO-US015849

15-JUL-1998; 15-JUL-1998; 15-JUL-1998; 98US-0092921P. 98US-0092922P. 98US-0092956P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, F Lafleur DW, Mucenski M, Komatsoulis G, Duan RD, Rosen CA, , Ebner R, Olsen HS, Brewer LA, | , Endress GA, Soppet DR; , Moore PA, Florence KA, Shi Y; PE;

WPI; 2000-161128/14. N-PSDB; AAZ98094.

New isolated human genes, useful for diagnosis and treatment of, e.g. cancers, neurological or blood disorders.

Claim 11; Page 429; 494pp; English

The polynucleotide sequences given in AAZ98017 to AAZ98108 encode the

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RESULT 2
AABO6118
ID AABO
XX AABO
XX AABO
XX Huma
XX Huma
XX Huma
XX Huma
XX Hoet
KW Foet
KW Pari
KW WO2
XX 113-
XX 113-
XX 113-
XX 113-
XX 114-
XX 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; Jastrointestinal disorder; altergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; gene therapy; chromosome 19.
                                                                                                                                                               13-JAN-2000; 2000US-00482273.
                                                                                                                                                                                                                                          12-JAN-2001; 2001WO-US000911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene 14 encoded secreted protein HAUAI83, SEQ ID NO:180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted proteins given in AAY87064 to AAY87223. Human so
in can have activities based on the tissues and cells the
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/label= Mature_human_secreted_protein
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
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Pred. No. 2.9e-30;
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CC ameliorating medical conditions, e.g., by protein or gene therapy.

CC ameliorating medical conditions, e.g., by protein or gene therapy.

CC new protein in a sample or by determining the presence of mutations in

CC the new genes. Specific uses are described for each of the 71 genes,

CC based on the tissues in which they are most highly expressed, and include

CC disorders, cancer, tunours, foetal and developmental abnormalities,

CC disorders (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune

CC cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease),

CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,

CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,

CC proliferation, to prevent skin aging due to sunburn, to mainteain organs

CC proliferation, to prevent skin aging due to sunburn, to mainteain organs

CC partners, and in chemotaxis, and can be used as a food additive or

CC preservative to modify storage properties. Antibodies specific for a

CC protein of the invention can be used in alleviating symptoms associated

CC with the disorders mentioned above, and in disgnostic immunoassays e.g.,

CC present sequence represents a human secreted protein of the invention
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted protein genes, and AAB06041-AAB06132 represent the proteins they encode. AAB06133 represent human secreted protein fragments. The secreted proteins and their genes are useful for preventing, treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 796; 864pp; English.
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I, Olsen HS, Bru
L, Muscenski M,
  AA;
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wer LA, Florence KA,
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Young PE,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
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100.0%; Pred.
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No. 2.9e-30;
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Length 49;

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rheumatoid arthritis, hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; cardiovascular disorder; pastem disorder, Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging;

cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm;

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ABR47655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC secreted protein (and its fragment, domain, epitope, variant, excetted command species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell control of the secreted protein. The nucleic acid and protein are used to gartner of the secreted protein. The nucleic acid and protein are used to grevent, diagnose, treat or ameliorate a medical condition in e.g. cc humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for cexample aucoimmune diseases e.g. rheumatoid arthritis, hyperproliferative cd isorders e.g. neopleasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, cc angiogenesis, nervous system disorders e.g. Alzheimer's disease, cc e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing can epithelial cell proliferation, to prevent skin aging due to subsurn, co maintain organs before transplantation, for supporting cell culture of polypeptides can also be used to aid wound healing confirmary tissues, to regenerate tissues and in chemotaxis. The cc polypeptides can also be used to aid wound healing confirmate tissues and in chemotaxis. The cc polypeptides can also be used to aid wound healing confirmate tissues and in chemotaxis. The cc polypeptides can also be used to aid wound healing confirmate tissues and in chemotaxis. The cc polypeptides can also be used to aid wound healing confirmate tissues and in chemotaxis. The cc polypeptides can also be used to aid wound healing to maintain organs before transplantation, for supporting cell culture of confirmate tissues and in chemotaxis. The confirmate to a novel human secreted protein of the invention
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Best Local Similarity
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  Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human
                                                                                                           12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 1273; 1478pp; English
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Endress GA,
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12-JAN-2001; 2001WO-US000911.
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                                                                  Human secreted protein, SEQ ID 546.
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Mucenski
                                                                                                           (first
                                                                                                             entry)
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lorence KA,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolism. Note: The sequence data for this electronic format and is available from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted proteins, useful diagnosing, prognosticating, treating disorders such as arrhythmia.
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19-JUL-2001; 2001US-0306171P
13-NOV-2001; 2001US-0331287P
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                                                                                                                                                                                       ABR00022;
                                                                                                                                                                                                                                       ABR00022 standard; protein; 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 260; DB 6; ilarity 100.0%; Pred. No. 2.9e-30; Conservative 0; Mismatches 0;
                                                                                                                                  (first entry)
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and/or ameliorating cardiovascular
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Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver;

Human gene 12 encoded secreted protein HAUAI83, SEQ ID NO:311.

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RESULT 6
ADB91468
ID ADB9
XX ADB9
XC ADB9
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AC ADB9
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C ADB9
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Best Local (
                Secreted protein;
                                                                         Human secreted protein #SEQ ID 414.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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gene therapy; antidiabetic; diabetes; human.
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Pred. No. 2.9e-30;
Mismatches 0;
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Best Local S
Matches 49
                                                                                                                                       antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antidiabetic; immunosuppressive; dermatological; nephrotropic; antiparkinsonian; neuroprotective; neuroprotective; nubaccerial; virucide; fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic; haemopoietic; haematologic; anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes;
                                                                            systemic lupus erythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein - SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC74024 standard; protein; 49
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19-JUL-2001;
13-NOV-2001;
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                                                          bacterial; viral; fungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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g diabetes or c
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2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM;
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Pred. No. 2.9e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
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                                                        Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; dovelopmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer; sitsease; restenceis; AIDS; cognitive disorder; schirophrenia; prostate; obseity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human secreted polypeptide for diagnosing, preventing or treating hematopoletic or hematologic disorders (e.g. anemia), autoinmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                             regulation; malabsorption; gastritis;
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Pred. No. 2.9e-30;
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Best Loc Matches Query Match Best Local

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Pred. No. 3e-30; Mismatches 0

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cione detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AXX00602) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AXX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the proposed by the protein of the specific pathological conditions can be diagnosed by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the
                                                                                                                                                                                                                                                                                                                                           Young P, Florence
                                                                                                                                                                                                                                    New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                   This sequence represents a secreted human protein encoded by the gene
                                                                                                                                                                                                                                                                                         WPI; 1999-070066/06.
N-PSDB; AAX00677.
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                          described uses)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 cc dermal papilla, human keratinocytes and meonatal foreskin fibroblasts, cc and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cc cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate stimulate to thinding of HIV-1 to leukocytes. The invention may also be used to treat corowth and developmental defects, skin wounds and hair follicle crowth and developmental defects, skin wounds and hair follicle crowth and developmental defects, skin wounds and hair follicle corowth and developmental defects, skin wounds and hair follicle crowth and sequences AAY75942-Y76123 represent polypeptides encoded by counces AAY75942-Y75147, AAY76020-Y76021, AAY76094-Y76104 and AAY76119 counce generies AAY75942-Y75989, AAY76021, AAY76071, AAY76106-Y776109 and AAY76112 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y776109 and AAY76112 are proteins with one or more putative transmembrane
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 185; 235pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1998;
09-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1999;
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                                                                                                                                                                                                                                               Local Similarity
mes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates
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                                                                                                                                                                                                                                               Conservative
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98US-00188930.
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                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                         Score 260; DB 3;
Pred. No. 4.3e-30;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                             Length
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RESULT 11
AABCO654
ID AABCO6
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                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                          The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenests, inhibiting angiogenests and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                          AAE06054
                                                                                                                                                                                                                                                                                                           Sequence 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating i disease, cancer and neurological diseases.
                                                                                                                                                                                                                                                                                                                                     oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 251; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-007495/01
                                                                                                                                                                                                                                                         49;
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n дс;
                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                       MILLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
                                                                                                                                       standard; protein;
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                                                                                                                                                                                                                                                       100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                   examining
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                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                      Score 260; DB 4;
Pred. No. 4.3e-30;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                   expression
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                                                                                                                                                                                                                                                                                                                                   patterns
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                                                                                                                                                                                                                                                                              Length 70;
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Human; secreted protein; proliferative disorder; cancer; tumour; asthma foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; hIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;

24-SEP-2001

(first

entry)

AAE06054;

Human gene

14 encoded secreted protein HHEPG41,

SEQ ID NO:116.

psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive;

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cc new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, can based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative cc disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune cdisorders, cancers, timours, foetal and developmental abnormalities, cancers, tumours, foetal and developmental abnormalities, commune control of proliferative commune control of proliferative commune communes are most in the immune system, AIDS, autoimmune communes, cancers, allergies, and include communes communes, and insorders, disease of the immune system, AIDS, autoimmune communes, and insorders, disease of the immune system, AIDS, autoimmune consists, as a control of communes, and insorders, and insorders, and infections. The compliancy-related disorders, and corine disorders, and infections. The compliancy-related disorders, endocrine disorders, and infections. The consists of the insorders, to identify their cognate ligands or binding corresponding to the insorders as and in chemotaxia, and can be used as a food additive or properties of the invention can be used in alleviating symptoms associated control of the invention can be used in alleviating symptoms associated control sequence represents a human secreted protein of the invention can be used in managenesis. The invention can be used in alleviating symptoms associated control sequence represents a human secreted protein of the invention.
  Query Match
Best Local S
Matches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-425865/45
N-PSDB; AAD11643.
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                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafleur DW,
Endress GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding in preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-2001; 2001WO-US000911
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    49;
                      Similarity
                                                                                70 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 747; 864pp; English.
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, Olsen HS, Bre
, Muscenski M,
    Conservative
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/label Signal peptide
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                      100.0%;
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M, Ebner R;
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wer LA, Florence KA,
    0
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Pred.
    Mismatches
e 260; DB 4;
. No. 4.3e-30;
smatches 0;
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Young PE,
                                     Length
    Indels
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Lafleur

SM, DW,

Komatsoulis G, Olsen H, B Mucenski M,

Brewer LA, M, Ebner R;

Duan DR, Rosen CA, wer LA, Florence KA,

Moore PA, Young PE,

Soppet DR;

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MILLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
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rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder, Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
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fungicide; opthalmalogical; autoimmune disease; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein encoded by gene 14 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG33876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG33876 standard; protein;
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25-SEP-2000; 2000US-0234925P. 12-JAN-2001; 2001WO-US000911. 24-SEP-2001; 2001WO-US029871. (HUMA-) HUMAN GENOME SCI INC

Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis, WPI; 2002-362489/39. N-PSDB; ABK69739.

Claim 11; Page 1228; 1478pp; English

CC fragment, homologue complement or allelic variant) encouring a human CC secreted protein (and its fragment, domain, epitope, variant secreted CC form and species variant). Also included are a recombinant vector CC comprising the nucleic acid, a recombinant host cell comprising the secreted protein are recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell comprising the secreted protein. The nucleic acid and protein are used to partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for CC example autoimmune diseases e.g. rhaumatoid arthritis, hyperproliferative CC eisorders e.g. neoplasms of the breast or liver, cardiovascular disorders CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, CC infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infection. Many other diseases and disorders are listed in CC e.g. pecification. The polypeptides can also be used to aid wound healing can epithelial cell proliferation, to prevent skin aging due to sunburn, CC to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The collypeptides can also be used as a food additive or preservative to circusase or decrease storage capabilities. The preservative to The invention relates to an isolated nucleic acid molecule (or its

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ARBSTLT 13
ABB72197
ID ABB72
XX ABB72
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XX ABB72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB72197;
                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in meantainting tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-122020/16
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25-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental defect;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB72197 standard;
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 207; 466pp; English.
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49; Conserv
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MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
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al defect; inflammatory disease; dermatological; vulnerary;
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                                                                                              Conservative
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2000US-0221232P.
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Pred. No. 4.3
0; Mismatches
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Pred.
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No. 4.3e-30;
                                                                                                                       260; DB 5;
No. 4.3e-30;
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RESULT 14
                             The polymucleotide sequences given in AAZ98017 to AAZ98108 encode the CC protein can have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; antiinflammatory; nootropic; neuroprotective; and ccl minumosuppressive; antiinflammatory; nootropic; neuroprotective; and cc polymeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polymeptides in a can be diagnosed by determining the amount of the new polypeptides in a complete or by determining the presence of mutations in the new cc polymucleotides. Human secreted protein s and their polymucleotides can be used for developing products for the diagnosis or treatment of cancer, be used for developing products for the diagnosis or treatment of cancer, cc polymucleotides. Human secreted protein s and their polymucleotides can complymucleotides, blood disorders, diseases of the immune system, cc autoimmune diseases, hepatic and renal disease, inflammation, allergies, and cc disbetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, cc arbtritis, infections, AIDS, spinal cord injuries, transplant rejection, cc diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, can also be used and metabolic disorders. The proteins or polymucleotides can also be used cod additives or preservatives. The proteins are also useful for sequence used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM, A
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15-JUL-1998;
15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; arthritis; autoimmune disease; hepatic disease; renal disease; inflammation; alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; infection; AIDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; reproductive disorder; gastrointestinal disorder; respiratory disorder; reproductive disorder; gastrointestinal disorder; respiratory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY87077 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolic disorder; food additive; preservative; chromosome
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, Ebner R, Olsen HS,
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Endress GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INC.
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en HS, Brewer LA,
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lorence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of,
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71 AA;

Length 71;

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AAY59659
ID AAY59
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XX AAY59
XX Becre
KW Secre
KW Secre
KW Chrom
KW hyper
XX Chrom
XX PD 12-AU
XX 09-FE
XX 04-SE
PR 10-AU
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XX Claim
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                                                                                                             This sequence represents a human secreted protein of the invention. The coxtended CDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative identification by DNA sequencing. They may also be used in the proteins encoded by the extended cDNAs are useful in identification of tissue specific continue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. Signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter of several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and relative dispassed in turn and interval.
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Best Local (
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13-APR-1998;
10-AUG-1998;
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Sequence 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extended cDNAs useful for expressing specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-600966/51.
N-PSDB; AAZ40787.
                                                           rheumatic diseases, embryogenic disorders, hypertension, renal inju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 191; 244pp; English.
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98US-0081563P.
98US-0096116P.
98US-0099273P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB000282
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Pred. No. 4.4e-30;
Mismatches 0;
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Query Match

100.0%; Score 260;

DB 2;

Length 106;

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37 MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
                1 MNLLGMIFSMCGLMLKLKWCAWVAVYCSFISFANSRSSEDTKQMMSSFM
                                           Conservative 0;
                                            Pred. No. 6.
                                             . 6.9e-30;
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